

STIC-Biotech/ChemLib

72025

From: Maupin, Christine
Sent: Monday, July 29, 2002 6:46 PM
To: STIC-Biotech/ChemLib
Subject: application 10/014743

Sensitivity: Private

could I please have the 3 sequences for application 10/014743 search in all data bases
thank you
Christine

Christine Maupin Ph.D
Patent Examiner
Technology Center 1600
(Biotechnology)
Art Unit 1637
Building CM1 Room 10A16
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Fax: 703-746-7641

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

CRIE

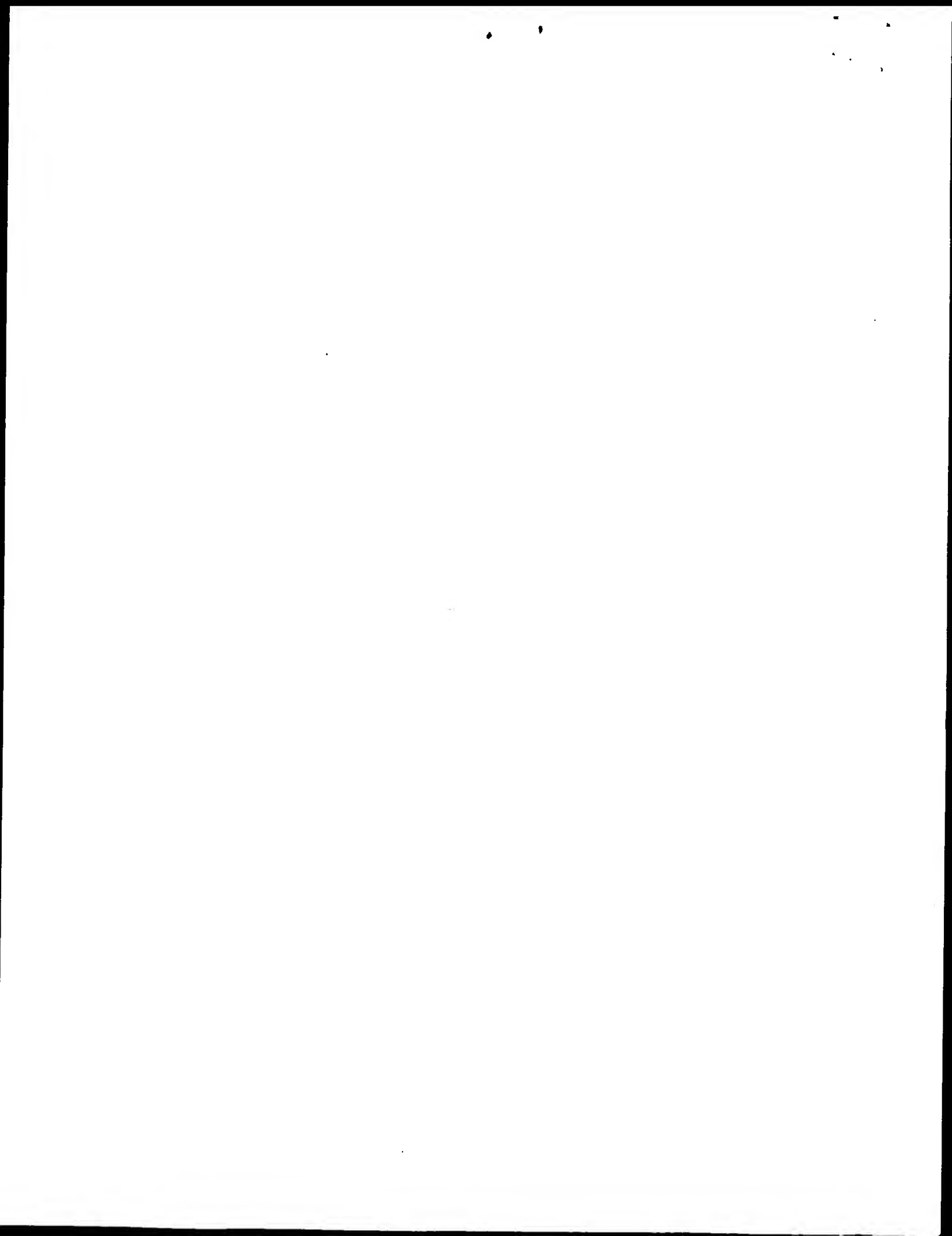
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TYPE OF SEARCH:

NA Sequences: _____
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Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

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08-02-02
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Number of Databases: 1

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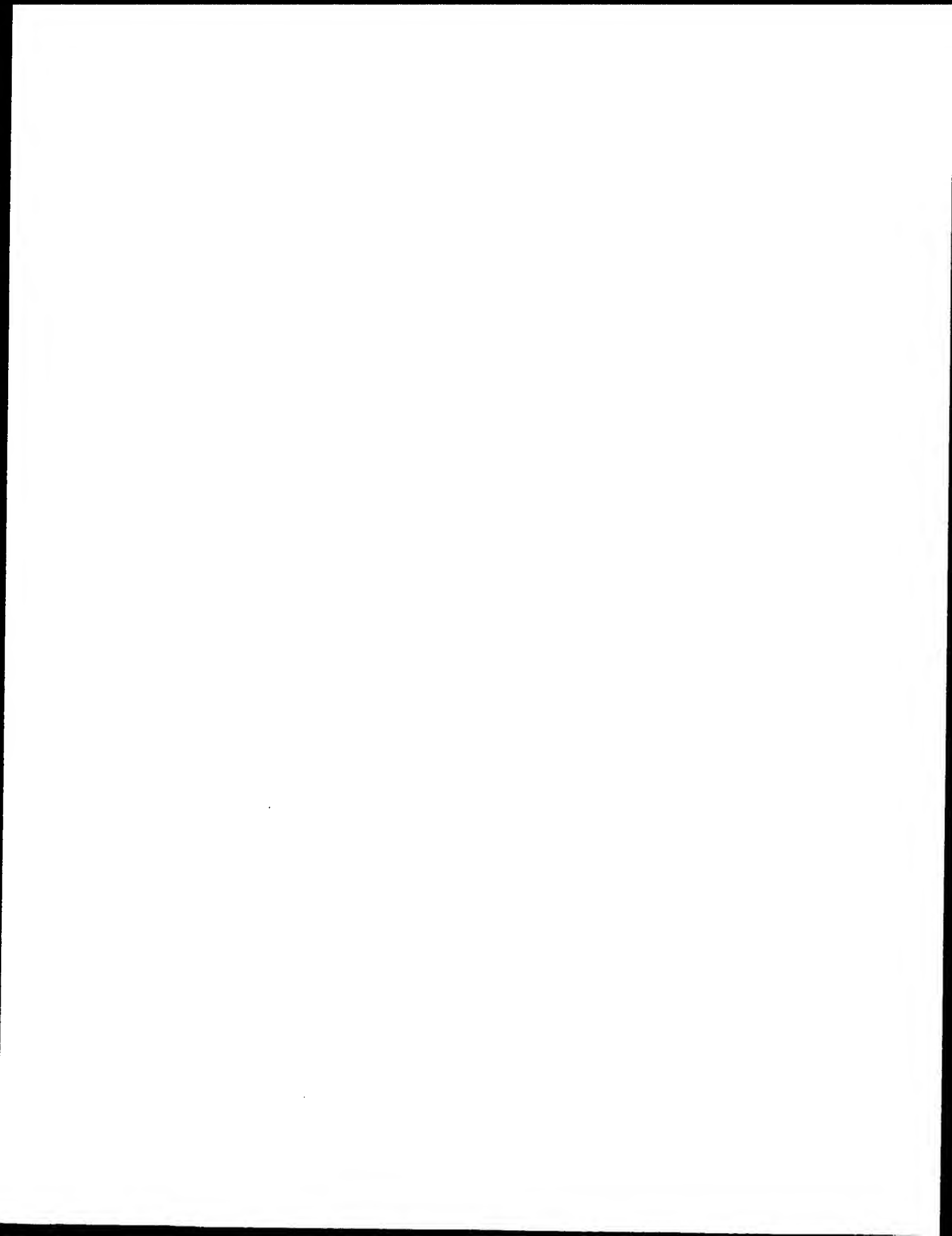
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____ Geninfo
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☒ Other CGN



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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:50:09 ; Search time 4897.61 Seconds
(without alignments)
5376.025 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1217	100.0	1217	11	US-08-726-462A-1	Sequence 1, Appl
3	1217	100.0	1217	37	US-10-014-743-1	Sequence 1, Appl
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RESULT 2
US-08-726-462A-1
; Sequence 1, Application US/08726462A
; GENERAL INFORMATION:
; APPLICANT: Perkins-Elmer Corporation, Applied Biosystems
; APPLICANT: Division ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESS: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for Windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,462A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462A-1
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Db 1201 CATTCTGGCCACACAG 1217

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; Sequence 1, Application US/10014743
; GENERAL INFORMATION:
; APPLICANT: PE Corporation (NY)
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
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; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; APPLICATION NUMBER: 09/272,097
; FILING DATE: March 18, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 493-9300
; TELEFAX: (650) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Db 1021 TTGCGCTGAGTAGAGNACTCAAACTATCGGCTTGTGTTATATCCAGAACAAATATAC 1080
QY 1081 CCCCAGCCATTGCAACAGGAAAAACGCTCATGGAATACCTACATTTTACCGCTCAATCG 1140
Db 1081 CCCCAGCCATTGCAACAGGAAAAACGCTCATGGAATACCTACATTTTACCGCTCAATCG 1140
QY 1141 TCTGAAATGGATTATTTACATTGGCAGATTCCAGTTCACAGCAGGTAATAAAGGGA 1200
Db 1141 TCTGAAATGGATTATTTACATTGGCAGATTCCAGTTCACAGCAGGTAATAAAGGGA 1200
QY 1201 CATTCTGCCCAACAGAG 1217
Db 1201 CATTCTGCCCAACAGAG 1217

```

PCT-US93-10850-1/c
; Sequence 1, Application PC/TUS9310850
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10850
; FILING DATE: 10-NOV-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: FP-IX 9769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ. ID NO: 1:
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; PCT-US93-10850-1

Query Match 94.6%; Score 1150.8; DB 1; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGGTCATAGCTGTTTCCCTGTGTGAAATGTTATCCGCTCACAATTTCCACACAACAT 123
DB 6226 ATCTGGTCATAGCTGTTTCCCTGTGTGAAATGTTATCCGCTCACAATTTCCACACAACAT 6167

QY 124 ACGAGCCGGAAGCATAAAGCTGTAAGCCCTGAGCCCTGAGCCCTGAGAGAGATT 183
DB 6166 ACGAGCCGGAAGCATAAAGCTGTAAGCCCTGAGCCCTGAGCCCTGAGAGAGATT 6107

QY 184 AATTCGGTTGCGCTCACTCCGCTTCCAGTCGGGAAACCTGTCGTCGAGCTGCAATTA 243
DB 6106 AATTCGGTTGCGCTCACTCCGCTTCCAGTCGGGAAACCTGTCGTCGAGCTGCAATTA 6047

QY 244 ATGAATCGGCCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGCGCCAGGGTGGTTTTTC 303
DB 6046 ATGAATCGGCCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGCGCCAGGGTGGTTTTTC 5987

QY 304 TTTTCACAGTGAGAGCGGCAACAGCTGATTCCTTCCAGCTGAGCCCTGAGAGAGATT 363
DB 5986 TTTTCACAGTGAGAGCGGCAACAGCTGATTCCTTCCAGCTGAGCCCTGAGAGAGATT 5927

QY 364 GCAGCAGCGGTCACAGCTGTTTTCGCTTCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 423
DB 5926 GCAGCAGCGGTCACAGCTGTTTTCGCTTCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 5867

QY 424 CGAAATCGGCAAAATCCCTTATTAATCAAAAGATACCCGAGATAGGTTGAGTGTGT 483
DB 5866 CGAAATCGGCAAAATCCCTTATTAATCAAAAGATAGGTTGAGTGTGTGT 5807

DB 5866 CGAAATCGGCAAAATCCCTTATTAATCAAAAGATAGGTTGAGTGTGTGT 5807
QY 484 TCCAGTTTGGAAACAAGAGTCCACTATTAAAGAAGTGGACTCCACAGTCAAGAGCGGAAA 543
DB 5806 TCCAGTTTGGAAACAAGAGTCCACTATTAAAGAAGTGGACTCCACAGTCAAGAGCGGAAA 5747
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DB 5746 AACCGCTCTATCAGCGCGGATGCGCCACTACGTGAACCATCAGCCAAATCAAGTTTTTGGG 5687
QY 604 GTCGAGGTGCGGTAAAGCACTAAATTCGGAACCTTAAGAGGAGCCGCCGATTTAGAGCTTG 663
DB 5686 GTCGAGGTGCGGTAAAGCACTAAATTCGGAACCTTAAGAGGAGCCGCCGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCCGCGGCAACGTGGCGAGAAAGGAAGGAAAGCAAGAGGAGCGGCGC 723
DB 5626 ACGGGGAAAGCCGCGGCAACGTGGCGAGAAAGGAAGGAAAGCAAGAGGAGCGGCGC 5567
QY 724 TAGGCGCTGGCAAGTGTAGCGGTGACGCTGCGGTAAACACACACACCGCGCGCTTAA 783
DB 5566 TAGGCGCTGGCAAGTGTAGCGGTGACGCTGCGGTAAACACACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGCGCGGCTACTATGGTGTGCTTACGAGCAGGTAAAGTCTTTCCT 843
DB 5506 TCGCGCGCTACAGCGCGGCTACTATGGTGTGCTTACGAGCAGGTAAAGTCTTTCCT 5447
QY 844 CGTTGGAAATCAGAGCGGGAGCTAAACAGGAGCGCGGATTAAGAGGATTTAGACAGGAACG 903
DB 5446 CGTTGGAAATCAGAGCGGGAGCTAAACAGGAGCGCGGATTAAGAGGATTTAGACAGGAACG 5387
QY 904 GTACGCCAGAATCTTGAAGAGTGTGTTTATATCATGTAGGCGCACCGAGTAAAGAGTCT 963
DB 5386 GTACGCCAGAATCTTGAAGAGTGTGTTTATATCATGTAGGCGCACCGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTCATAGTAAATACATCACTTG 1023
DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTCATAGTAAATACATCACTTG 5267
QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCGCTTGTGTAATATCAGAACATATTACCGC 1083
DB 5266 CTTGAGTAGAAGAACTCAAACTATCGGCGCTTGTGTAATATCAGAACATATTACCGC 5207
QY 1084 CAGCCATTCAGACAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 1143
DB 5206 CAGCCATTCAGACAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 5147
QY 1144 GAAATGGATTATTTACATTTGCGAGATTCACAGTTCACACGACAGTAAATAAGGAGAT 1203
DB 5146 GAAATGGATTATTTACATTTGCGAGATTCACAGTTCACACGACAGTAAATAAGGAGAT 5087

RESULT 5
PCT-US93-10850-5/c
; Sequence 5, Application PC/TUS9310850
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

[illegible]

964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCATTG 1023
5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCATTG 5267
1024 CTTGAGTGAAGAACTCAAACTATCGGCTTGTGTGTAATATCCAGCAATATTACCGC 1083
5266 CTTGAGTGAAGAACTCAAACTATCGGCTTGTGTGTAATATCCAGCAATATTACCGC 5207
1084 CAGCATTTGCAACAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 1143
5206 CAGCATTTGCAACAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 5147
1144 GAAATGATTATTATACATTTGCGAGATTACACAGTCACACGACGACGATTAATAAGGGGACAT 1203
5146 GAAATGATTATTATACATTTGCGAGATTACACAGTCACACGACGACGATTAATAAGGGGACAT 5087
1204 TCTGCCCAACAGAG 1217
5086 TCTGCCCAACAGAG 5073

RESULT 7
US-08-150-740-5/C
; Sequence 5, Application US/08150740
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/150,740
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-IX 9796
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-150-740-5

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

64 ATCATGTGCTATAGCTGTTTCTGCTGAAATGTTATCCGCTCAAAATTCACACACAT 123
6226 ATCTGGTGCATAGCTGTTTCTGCTGAAATGTTATCCGCTCAAAATTCACACACAT 6167

64 ATCATGTGCTATAGCTGTTTCTGCTGAAATGTTATCCGCTCAAAATTCACACACAT 123
6226 ATCTGGTGCATAGCTGTTTCTGCTGAAATGTTATCCGCTCAAAATTCACACACAT 6167
124 ACAGCCGGAAGCATAAAGTGTAAAGCCCTGGGGTCCCTAAATGAGTGAGCTAACTCACAT 183
6166 ACAGCCGGAAGCATAAAGTGTAAAGCCCTGGGGTCCCTAAATGAGTGAGCTAACTCACAT 6107
184 AATGTGCTGCTACTGCCCGCTTCCAGTCGGGAACCTGCTGCTCCAGCTCAATTA 243
6106 AATGTGCTGCTACTGCCCGCTTCCAGTCGGGAACCTGCTGCTCCAGCTCAATTA 6047
244 ATCAATCGGCAACGCGGGGAGAGCGGTTTGGCTATTTGGCGCGCAGGGTGGTTTC 303
6046 ATCAATCGGCAACGCGGGGAGAGCGGTTTGGCTATTTGGCGCGCAGGGTGGTTTC 5987
304 TTTTACCAGTGTAGAGCGGCAACAGTGATTTGCCCTTACCCTGCTCCGCTGAGAGAGTT 363
5986 TTTTACCAGTGTAGAGCGGCAACAGTGATTTGCCCTTACCCTGCTCCGCTGAGAGAGTT 5927
364 GCAGCAGCGCTCCAGCTGTTTGGCCCGAGAGCGGTTTGGCTATTTGGCGCGCAGGGTGGTTTC 423
5926 GCAGCAGCGCTCCAGCTGTTTGGCCCGAGAGCGGTTTGGCTATTTGGCGCGCAGGGTGGTTTC 5867
424 CGAATCGGCAAAATCCCTTATTAATCAAAAGATAGCCCGAGATAGGTTGAGTGT 483
5866 CGAATCGGCAAAATCCCTTATTAATCAAAAGATAGCCCGAGATAGGTTGAGTGT 5807
484 TCCAGTTTGGAGCAAGAGTCCACTATTAAAGAACGTGAGCTCCCAACGTCAAAAGGCGAAA 543
5806 TCCAGTTTGGAGCAAGAGTCCACTATTAAAGAACGTGAGCTCCCAACGTCAAAAGGCGAAA 5747
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5746 AACGCTCTATCAGGCGGATGCCCTACCTACGTGAACCATCAACCAATCAAGTTTGGG 5687
604 GTCGAGGTCGCTAAGCACTAAATCGAAGCCTAAAGGGAGCGCCCGATTTAGAGCTTG 663
5686 GTCGAGGTCGCTAAGCACTAAATCGAAGCCTAAAGGGAGCGCCCGATTTAGAGCTTG 5627
664 ACAGGGAAGCGCGGAGAGCTGGCGGAGAAAGAGGAGAAAGCGAAAGAGCGCGCGC 723
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784 TGGCGCGCTACAGGCGCGCTACTGATGTTGCTTTGACGAGCAGTATACGCTGCTTCT 843
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844 CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGGCTTAAAGGATTTTAGACAGGAACG 903
5446 CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGGCTTAAAGGATTTTAGACAGGAACG 5387
904 GTAGCCAGAAATCTTGAGAGAGTGTGTTTATATATAGTGAGGCGCACCGAGTAAAGAGTCT 963
5386 GTAGCCAGAAATCTTGAGAGAGTGTGTTTATATATAGTGAGGCGCACCGAGTAAAGAGTCT 5327

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-150-740-1

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 ACGAGCCGGAAGCATAAAGTAAAGCTGGGTGCTAATGAGTGAGCTAACCTACATT 183
 Db 6166 ACGAGCCGGAAGCATAAAGTAAAGCTGGGTGCTAATGAGTGAGCTAACCTACATT 6107
 QY 184 AATTCGGTTCGCTCAGTCCCGCTTTCAGTGGGAAACCTGCTGCGCAGCTGATTA 243
 Db 6106 AATTCGGTTCGCTCAGTCCCGCTTTCAGTGGGAAACCTGCTGCGCAGCTGATTA 6047
 QY 244 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCGAGGGTGGTTTC 303
 Db 6046 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCGAGGGTGGTTTC 5987
 QY 304 TTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCCAGCCCTGGCCCTGAGAGATT 363
 Db 5986 TTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCCAGCCCTGGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGTGCACCGTGTGGTCCCGCAGCGGCAAAATCCTGTTGATGGTGGTTC 423
 Db 5926 GCAGCAAGCGTGCACCGTGTGGTCCCGCAGCGGCAAAATCCTGTTGATGGTGGTTC 5867
 QY 424 CGAAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
 Db 5866 CGAAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
 QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGACGTGAGTCCACAGCTCAAGGGCGGAAA 543
 Db 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGACGTGAGTCCACAGCTCAAGGGCGGAAA 5747
 QY 544 AACCGTCTATCAGGGGATGGCCCACTAGTGAACCATCACCCAAATCAAGTTTGGG 603
 Db 5746 AACCGTCTATCAGGGGATGGCCCACTAGTGAACCATCACCCAAATCAAGTTTGGG 5687
 QY 604 GTGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGTTG 663
 Db 5686 GTGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGTTG 5627
 QY 664 ACGGGAAAGCGCGGAGTGTAGCGGTACGCTGCGGCTTAAGGAGAGCAAGAGGAGCGGCG 723
 Db 5626 ACGGGAAAGCGCGGAGTGTAGCGGTACGCTGCGGCTTAAGGAGAGCAAGAGGAGCGGCG 5567
 QY 724 TAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGGCTTAAGGAGAGCAAGAGGAGCGGCG 783
 Db 5566 TAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGGCTTAAGGAGAGCAAGAGGAGCGGCG 5507
 QY 784 TCGCGCTACAGGCGGCTATGTTGTTTTCAGCAGACGATATAACGTTCTTCT 843
 Db 5506 TCGCGCTACAGGCGGCTATGTTGTTTTCAGCAGACGATATAACGTTCTTCT 5447
 QY 844 CTTTGAATCAGAGCGGAGCTTAAACAGAGCGGCTTAAAGGAGATTTAGACGAAG 903
 Db 5446 CTTTGAATCAGAGCGGAGCTTAAACAGAGCGGCTTAAAGGAGATTTAGACGAAG 5387
 QY 904 GTACGCCAGAACTTGAGAAGTGTATTAATCAGTGAAGCGCCAGCGAGTAAAGAGTCT 963
 Db 5386 GTACGCCAGAACTTGAGAAGTGTATTAATCAGTGAAGCGCCAGCGAGTAAAGAGTCT 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTTCTTTGATTAATACATCACTTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTTCTTTGATTAATACATCACTTG 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCCCTTGTGTTGATTAATACAGCAATATTACCG 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCCCTTGTGTTGATTAATACAGCAATATTACCG 5207
 QY 1084 CAGCCATTGCAACAGGAAACCTCATGGAATACCTACATTTTACGCTCAATCGCT 1143
 Db 5206 CAGCCATTGCAACAGGAAACCTCATGGAATACCTACATTTTACGCTCAATCGCT 5147
 QY 1144 GAATGGATTATTTACATTTGGCAGATTCACAGTCAACAGCAAGTAAATAGGAGCAT 1203
 Db 5146 GAATGGATTATTTACATTTGGCAGATTCACAGTCAACAGCAAGTAAATAGGAGCAT 5087
 QY 1204 TCTGGCCAAACAGAG 1217

Db 5086 TCTGGCCAAACAGAG 5073

RESULT 8

US-08-440-787-1/c
 ; Sequence 1, Application US/08440787
 ; GENERAL INFORMATION:
 ; APPLICANT: HUSE, WILLIAM D.
 ; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
 ; CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CAMPBELL AND FLORES
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/440,787
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/978,893
 ; FILING DATE: 10-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOSKI, ANTOINETTE F.
 ; REGISTRATION NUMBER: 34,202
 ; REFERENCE/DOCKET NUMBER: P-IX 9382
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-535-9001
 ; TELEFAX: 619-535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ; US-08-440-787-1

Query Match 94.6%; Score 1150.8; DB 8; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGGTCATAGCTGTTTCTGTTGAAATTTCTTATCCGCTCACAAATCCACACAAAT 123
 Db 6226 ATCTTGGTCATAGCTGTTTCTGTTGAAATTTCTTATCCGCTCACAAATCCACACAAAT 6167
 QY 124 ACGAGCCGGAACATTAAGTGAAGCCCTGGGTGCTAATGAGTGAGCTAACTCACTT 183
 Db 6166 ACGAGCCGGAACATTAAGTGAAGCCCTGGGTGCTAATGAGTGAGCTAACTCACTT 6107
 QY 184 AATTGCGTTGGCTCAGTCCCGCTTTCAGTCGGGAACCTGTGTCGCGCAGCTGCATTA 243
 Db 6106 AATTGCGTTGGCTCAGTCCCGCTTTCAGTCGGGAACCTGTGTCGCGCAGCTGCATTA 6047
 QY 244 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCGAGGGTGGTTTC 303
 Db 6046 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCGAGGGTGGTTTC 5987
 QY 304 TTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCCAGCCCTGGCCCTGAGAGATT 363
 Db 5986 TTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCCAGCCCTGGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGTGCACCGTGTGGTCCCGCAGCGGCAAAATCCTGTTGATGGTGGTTC 423

5926 GCAGCAAGCGGTCACGCTGGTTGGCCCGAGCGGCAAAATCCTGTTGATGGTGGTTC 5867
Db
QY 424 CGAATCGCAAAATCCCTATATAAATAAAGAAATACGCCGAGATAGGTTGAGTGTGT 483
Db 5866 CGAAATCGCAAAATCCCTATATAAATAAAGAAATACGCCGAGATAGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATATAAAGAAAGAGTCCCAACGTCGAAGGCGGAAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATATAAAGAAAGAGTCCCAACGTCGAAGGCGGAAA 5747
QY 544 ACCGCTCTATCAGGGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTGGG 603
Db 5746 AACCGCTCTATCAGGGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTGGG 5687
QY 604 GTCGAGTGGCTAAAGCACTAAATCGGAACCTTAAGGAGGCGCCCGATTTAGAGTTG 663
Db 5686 GTCGAGTGGCTAAAGCACTAAATCGGAACCTTAAGGAGGCGCCCGATTTAGAGTTG 5627
QY 664 ACAGGAAAGCGGCGAACGTTGGGAGAAAGGAAGGAAGCAAGGAGGCGGCG 723
Db 5626 ACAGGAAAGCGGCGAACGTTGGGAGAAAGGAAGGAAGCAAGGAGGCGGCG 5567
QY 724 TAGGCGCTGCAAGTGTAGCGTACGCTGCGGTAAACACACACCGCGCGCTTAA 783
Db 5566 TAGGCGCTGCAAGTGTAGCGTACGCTGCGGTAAACACACACCGCGCGCTTAA 5507
QY 784 TGCAGCGCTACAGGCGGCTACTATGTTGTTGAGAGCAGCTATAACGTGCTTCT 843
Db 5506 TGCAGCGCTACAGGCGGCTACTATGTTGTTGAGAGCAGCTATAACGTGCTTCT 5447
QY 844 CGTTGGAATCAGCGGAGCTAAACAGGAGCGGATTAAGGAGATTTAGACAGGAG 903
Db 5446 CGTTGGAATCAGCGGAGCTAAACAGGAGCGGATTAAGGAGATTTAGACAGGAG 5387
QY 904 GTACGCCAGATCTTGAGAGTGTATTAATCAGTGAAGCCACCGAGTAAAGAGTCT 963
Db 5386 GTACGCCAGATCTTGAGAGTGTATTAATCAGTGAAGCCACCGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACGTTGTAGCAATACTTCTTGTAGTAAATACATCACTTG 1023
Db 5326 GTCCATCAGCAAAATTAACGTTGTAGCAATACTTCTTGTAGTAAATACATCACTTG 5267
QY 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGTAATATCCAGAAATATACCG 1083
Db 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGTAATATCCAGAAATATACCG 5207
QY 1084 CAGCCATTGCAACAGGAAAGCGCTCATGGAATACCTACATTTGACGCTCAATGCTCT 1143
Db 5206 CAGCCATTGCAACAGGAAAGCGCTCATGGAATACCTACATTTGACGCTCAATGCTCT 5147
QY 1144 GAATGGATTTTACATTTGGCAGATTCACAGTCAACAGGAGCAATATAAGGAGCAT 1203
Db 5146 GAATGGATTTTACATTTGGCAGATTCACAGTCAACAGGAGCAATATAAGGAGCAT 5087
QY 1204 TCTGGCCAAACAGAG 1217
Db 5086 TCTGGCCAAACAGAG 5073

RESULT 9
US-08-440-787-5/c
; Sequence 5, Application US/08440787
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
; TITLE OF INVENTION: CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-IX 9382
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-440-787-5

Query Match 94.6%; Score 1150.8; DB 8; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 ATCATGCTCATAGCTGTTCTCTGTGAAATTTGTTATCCGCTCAAAATTCACACACAT 123
Db 6226 ATCTGCTCATAGCTGTTCTCTGTGAAATTTGTTATCCGCTCAAAATTCACACACAT 6167
QY 124 ACAGCGGGAAGCATAAAGTGTAAAGCTGGGTCCTTAAGTGAAGTGAAGTGAAGTGAAGT 183
Db 6166 ACAGCGGGAAGCATAAAGTGTAAAGCTGGGTCCTTAAGTGAAGTGAAGTGAAGTGAAGT 6107
QY 184 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
Db 6106 AATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6047
QY 244 ATGAATCGGCAACGCGCGGAGAGCGGTTTCGTTATTTGGGCGCAGGTTGTTTTC 303
Db 6046 ATGAATCGGCAACGCGCGGAGAGCGGTTTCGTTATTTGGGCGCAGGTTGTTTTC 5987
QY 304 TTTTCCAGCTGAGACGCGGCAACAGCTGATTCCTTCCAGCTGCGGCTGCGGCTGAGAGATT 363
Db 5986 TTTTCCAGCTGAGACGCGGCAACAGCTGATTCCTTCCAGCTGCGGCTGCGGCTGAGAGATT 5927
QY 364 GCAGCAAGCGGTCACAGCTGTTTTCGCGGCGAGAGCGGTTTCGTTATTTGGGCGCAGGTT 423
Db 5926 GCAGCAAGCGGTCACAGCTGTTTTCGCGGCGAGAGCGGTTTCGTTATTTGGGCGCAGGTT 5867
QY 424 CGAAATCGGCAAAATTCCTTTATTAATCAAAAGATAGCCGAGATAGGTTTCAGTGTGT 483
Db 5866 CGAAATCGGCAAAATTCCTTTATTAATCAAAAGATAGCCGAGATAGGTTTCAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATATAAAGAAAGAGTGAAGTGAAGTGAAGTGAAGT 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATATAAAGAAAGAGTGAAGTGAAGTGAAGTGAAGT 5747
QY 544 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTGGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTGGG 5687
QY 604 GTCGAGTGGCTAAAGCACTAAATCGGAACCTTAAGGAGGCGCCCGATTTAGAGTTG 663
Db 5686 GTCGAGTGGCTAAAGCACTAAATCGGAACCTTAAGGAGGCGCCCGATTTAGAGTTG 5627

Db 5386 GTACGCCAGAATCTTGAGAGGTGTTTATATACAGTGAGGCCACCGAGTAAAGAGTCT 5327
 Qy 964 GTCCATACGCAAAATTAACCGTTGTAGCAATCTTCTTTGATAGTAAATACATCACTTG 1023
 Db 5326 GTCCATACGCAAAATTAACCGTTGTAGCAATCTTCTTTGATAGTAAATACATCACTTG 5267
 Qy 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGATATCCAGAACAAATATTACCGC 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGATATCCAGAACAAATATTACCGC 5207
 Qy 1084 CAGCCATTCACAGGAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 1143
 Db 5206 CAGCCATTCACAGGAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 5147
 Qy 1144 GAAATGGATTTTACATTTGGAGATTCACAGCACAGCAGTAAATAAAGGGACAT 1203
 Db 5146 GAAATGGATTTTACATTTGGAGATTCACAGCACAGCAGTAAATAAAGGGACAT 5087
 Qy 1204 TCTGGCCACAGAG 1217
 Db 5086 TCTGGCCACAGAG 5073

RESULT 11

US-08-995-243-5/C
 ; Sequence 5, Application US/08995243
 ; GENERAL INFORMATION:
 ; APPLICANT: HUSE, WILLIAM D.
 ; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
 ; TITLE OF INVENTION: CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CAMPBELL AND FLORES
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/995,243
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/978,893
 ; FILING DATE: 10-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KONSIL, ANTOINETTE F.
 ; REGISTRATION NUMBER: 34,202
 ; REFERENCE/DOCKET NUMBER: P-IX 9382
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-535-9001
 ; TELEFAX: 619-535-8949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ; US-08-995-243-5

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 64 ATCATGGCTAGCTGTTCTTCTGTTGAAATGTTATCCGCTCAAAATTTCCACACAAACAT 123
 Db 6226 ATCCCTGGTCATAGCTGTTTCTGTTGAAATGTTATCCGCTCAAAATTTCCACACAAACAT 6167

Qy 124 ACAGCGCGAAGCATAAAGTGTAAAGCCTGGGTGCTTAAGTGTAGTGTAGCTAACTCACTT 183
 Db 6166 ACAGCGCGAAGCATAAAGTGTAAAGCCTGGGTGCTTAAGTGTAGTGTAGCTAACTCACTT 6107
 Qy 184 AATTGGCTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGTCAGCTGCATT 243
 Db 6106 AATTGGCTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGTCAGCTGCATT 6047
 Qy 244 ATGAATCGCCCAACGCGCGGGAGAGGGGTTTGGGTATTCGGGCGCCAGGGTGGTTTTC 303
 Db 6046 ATGAATCGCCCAACGCGCGGGAGAGGGGTTTGGGTATTCGGGCGCCAGGGTGGTTTTC 5987
 Qy 304 TTTTTCACAGTGAGACGGCAACAGCTGATTCGCCCTTCACCGCTTGGCCCTTGGAGAGTT 363
 Db 5986 TTTTTCACAGTGAGACGGCAACAGCTGATTCGCCCTTCACCGCTTGGCCCTTGGAGAGTT 5927
 Qy 364 GCAGCAAGCGGTCCAGCTGTTTGGCCAGCAGCGGAAATCCCTGTTGATGGTGGTTC 423
 Db 5926 GCAGCAAGCGGTCCAGCTGTTTGGCCAGCAGCGGAAATCCCTGTTGATGGTGGTTC 5867
 Qy 424 CGAAATCGGCAAAATCCCTTATATAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTCT 483
 Db 5866 CGAAATCGGCAAAATCCCTTATATAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTCT 5807
 Qy 484 TCCAGTTTGGCAACAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAGGGCGAAA 543
 Db 5806 TCCAGTTTGGCAACAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAGGGCGAAA 5747
 Qy 544 AACCGTCTATCAGGGCGATGGCCCTTACGTGAACCATCACCCAAATCAAGTTTGGTGG 603
 Db 5746 AACCGTCTATCAGGGCGATGGCCCTTACGTGAACCATCACCCAAATCAAGTTTGGTGG 5687
 Qy 604 GTGAGGTGCGTAAAGCACTAAATCGGAACCTTAAAGGAGGAGCCCGATTTAGAGCTTG 663
 Db 5686 GTGAGGTGCGTAAAGCACTAAATCGGAACCTTAAAGGAGGAGCCCGATTTAGAGCTTG 5627
 Qy 664 ACAGGAAAGCGCGGAGACGTGGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
 Db 5626 ACAGGAAAGCGCGGAGACGTGGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 5567
 Qy 724 TAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGGTACACACACACACACACACACAC 783
 Db 5566 TAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGGTACACACACACACACACACACAC 5507
 Qy 784 TCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATTAACGTGCTTCTCT 843
 Db 5506 TCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATTAACGTGCTTCTCT 5447
 Qy 844 CTTTGAATCAGAGCGGAGCTTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903
 Db 5446 CTTTGAATCAGAGCGGAGCTTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5387
 Qy 904 GTACGCCAGAATCTTGAGAGTGTGTTTATATAGTGTAGGCGCCAGGAGTAAAGAGTCT 963
 Db 5386 GTACGCCAGAATCTTGAGAGTGTGTTTATATAGTGTAGGCGCCAGGAGTAAAGAGTCT 5327
 Qy 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTTCTTTGATAGTAAATACATCACTTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTTCTTTGATAGTAAATACATCACTTG 5267
 Qy 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGATATCCAGAACAAATATTACCGC 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGATATCCAGAACAAATATTACCGC 5207
 Qy 1084 CAGCCATTCACAGGAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 1143
 Db 5206 CAGCCATTCACAGGAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 5147
 Qy 1144 GAAATGGATTTTACATTTGGAGATTCACAGCACAGCAGTAAATAAAGGGACAT 1203
 Db 5146 GAAATGGATTTTACATTTGGAGATTCACAGCACAGCAGTAAATAAAGGGACAT 5087

QY 1204 TCTGGCCACACAGAG 1217
 Db 5086 TCTGGCCACACAGAG 5073

RESULT 12

US-08-995-243A-1/c
 ; Sequence 1, Application US/08995243A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Soluble Peptides Having Constrained,
 ; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
 ; NUMBER OF INVENTION: Same.
 ; NUMBER OF SEQUENCES: 174
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/995,243A
 ; FILING DATE: 19-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/978,893
 ; FILING DATE: 10-NOV-1992
 ; APPLICATION NUMBER: US 08/440,787
 ; FILING DATE: 15-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IX 2955
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ; US-08-995-243A-1

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
 Best Local Similarity 99.8%; Pred. NO. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 64 ATCATGGTCATAGCTGTTCTGCTGTAATTTGTTATCGCTCACAATTCACACAACAT 123
 Db 6226 ATCTGGTTCATAGCTGTTTCTGCTGTAATTTGTTATCGCTCACAATTCACACAACAT 6167
 QY 124 ACAGCCGGAAGCATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATT 183
 Db 6166 ACAGCCGGAAGCATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATT 6107
 QY 184 AATTGCGTTGGCGTCACCTGCCGCTTCCAGTCGGGAACCTGCTGCGCCAGCTGCATTA 243
 Db 6106 AATTGCGTTGGCGTCACCTGCCGCTTCCAGTCGGGAACCTGCTGCGCCAGCTGCATTA 6047
 QY 244 ATGAATCGGCAACCGCGGGAGAGCGGTTTCGTTATTTGGCGCCAGGGTGGTTTTC 303
 Db 6046 ATGAATCGGCAACCGCGGGAGAGCGGTTTCGTTATTTGGCGCCAGGGTGGTTTTC 5987
 QY 304 TTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTACCAGCTGCCCTGAGAGATT 363
 Db 6046 TTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTACCAGCTGCCCTGAGAGATT 363

Db 5986 TTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTACCAGCTGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGGTCCACGCTGTTTCCCGCCAGCAGCGCAAAATCTCTTTGATGGTGGTTC 423
 Db 5926 GCAGCAAGCGGTCCACGCTGTTTCCCGCCAGCAGCGCAAAATCTCTTTGATGGTGGTTC 5867
 QY 424 CGAAATCGGCAAAATCTCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
 Db 5866 CGAAATCGGCAAAATCTCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
 QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGAAGCTGACCTCCAACTGCAAGGCGGAAA 543
 Db 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGAAGCTGACCTCCAACTGCAAGGCGGAAA 5747
 QY 544 AACCGTCTATCAGGCGGATGCCCACTACGTGAACCACTACCCCAAAATCAAGTTTGGG 603
 Db 5746 AACCGTCTATCAGGCGGATGCCCACTACGTGAACCACTACCCCAAAATCAAGTTTGGG 5687
 QY 604 GTGAGGTGCGGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 663
 Db 5686 GTGAGGTGCGGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 5627
 QY 664 ACGGGAAAGCGCGGCAACGTGGCGAAGAGGAGGAAAGCGGAGCGGCGC 723
 Db 5626 ACGGGAAAGCGCGGCAACGTGGCGAAGAGGAGGAAAGCGGAGCGGCGC 5567
 QY 724 TAGGGCGTGGCAAGTGTAGCGGTACGCTGCGCGTAAACACACACCGCGGCTTAA 783
 Db 5566 TAGGGCGTGGCAAGTGTAGCGGTACGCTGCGCGTAAACACACACCGCGGCTTAA 5507
 QY 784 TCGCGCGGTACAGGCGCGTACTAGTTGCTTTGACGAGCAGTATAACGTTTCCT 843
 Db 5506 TCGCGCGGTACAGGCGCGTACTAGTTGCTTTGACGAGCAGTATAACGTTTCCT 5447
 QY 844 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGGATTAAGGGATTTAGACAGAAAG 903
 Db 5446 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGGATTAAGGGATTTAGACAGAAAG 5387
 QY 904 GTAGCCCAAGATCTTGAGAGTGTATTAATCAGTGAGGCGCCAGTAAAGAGTGT 963
 Db 5386 GTAGCCCAAGATCTTGAGAGTGTATTAATCAGTGAGGCGCCAGTAAAGAGTGT 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAATACATCAGTGT 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAATACATCAGTGT 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCCAGAACAAATATACCGC 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCCAGAACAAATATACCGC 5207
 QY 1084 CAGCCATTGCAACAGGAAACCGCTCATGGAATACCTACATTTTACGCTCAATCGTCT 1143
 Db 5206 CAGCCATTGCAACAGGAAACCGCTCATGGAATACCTACATTTTACGCTCAATCGTCT 5147
 QY 1144 GAAATGGATTATTACATTTGGCAGATTTCACAGTCAACAGCAGCAATATAAGGGACAT 1203
 Db 5146 GAAATGGATTATTACATTTGGCAGATTTCACAGTCAACAGCAGCAATATAAGGGACAT 5087
 QY 1204 TCTGGCCACACAGAG 1217
 Db 5086 TCTGGCCACACAGAG 5073

RESULT 13
 US-08-995-243A-5/c
 ; Sequence 5, Application US/08995243A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Soluble Peptides Having Constrained,
 ; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
 ; NUMBER OF SEQUENCES: 174
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,243A
FILING DATE: 19-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: US 08/440,787
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-995-243A-5

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTCATAGCTGTTCTCTGTGTAAGTGTATCGGCTCACAATTCACACAAAT 123
DB 6226 ATCTGTTGTCATAGCTGTTCTCTGTGTAAGTGTATCGGCTCACAATTCACACAAAT 6167

QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTCCTTAATGAGTGAGCTAACTCACATT 183
DB 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTCCTTAATGAGTGAGCTAACTCACATT 6107

QY 184 AATTGCGTTGGCTCACTGCCGCTTTCCAGTCGGGAACCTGTCTGTCGCCAGCTGATTA 243
DB 6106 AATTGCGTTGGCTCACTGCCGCTTTCCAGTCGGGAACCTGTCTGTCGCCAGCTGATTA 6047

QY 244 ATGAATCGGCNACCGCGGGGAGAGCGGTTTGGTATGTCGGCCAGCGGTTTTC 303
DB 6046 ATGAATCGGCNACCGCGGGGAGAGCGGTTTGGTATGTCGGCCAGCGGTTTTC 5987

QY 304 TTTTCACAGTGAGAGCGGCAACAGCTGATTCCTTCCAGCTGCGCCCTGAGAGAGTT 363
DB 5986 TTTTCACAGTGAGAGCGGCAACAGCTGATTCCTTCCAGCTGCGCCCTGAGAGAGTT 5927

QY 364 GCAGCAAGCGTCCACGCTGTTGTCGCCAGAGGGAATTCCTGTTGATGCTGTTTC 423
DB 5926 GCAGCAAGCGTCCACGCTGTTGTCGCCAGAGGGAATTCCTGTTGATGCTGTTTC 5867

QY 424 CAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 483
DB 5866 CAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 5807

QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA 543
DB 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA 5747

QY 544 AACCGTCTATCAGGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGG 603

DB 5746 AACCGTCTATCAGGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGG 5687
QY 604 GTCGAGGTGCGGTAAAGCAGCTAAATCGGAAACCTTAAGGAGGCCCGCGGATTTAGAGCTTG 663
DB 5686 GTCGAGGTGCGGTAAAGCAGCTAAATCGGAAACCTTAAGGAGGCCCGCGGATTTAGAGCTTG 5627
QY 664 ACGGGAAAGCGCGGCAACCTGTCGAGAAAGGAAAGGAAAGGAAAGGAGGCGGCGC 723
DB 5626 ACGGGAAAGCGCGGCAACCTGTCGAGAAAGGAAAGGAAAGGAAAGGAGGCGGCGC 5567
QY 724 TAGGCGCTGGCAAGTGTAGCGGTACCGTGGCGGTAAACACACACACCGCGCGCTTAA 783
DB 5566 TAGGCGCTGGCAAGTGTAGCGGTACCGTGGCGGTAAACACACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGGCGCGTACTATGTTGCTTTCAGGAGCAGCTATTAACGCTTTCCT 843
DB 5506 TCGCGCGCTACAGGCGCGTACTATGTTGCTTTCAGGAGCAGCTATTAACGCTTTCCT 5447
QY 844 COTGGGAATCAGAGCGGGAGCTAAACAGGAGCGGATTAAGGAGTTTATAGACAGGACG 903
DB 5446 COTGGGAATCAGAGCGGGAGCTAAACAGGAGCGGATTAAGGAGTTTATAGACAGGACG 5387
QY 904 GTACGCCAGAACTTTGAGAAGTGTATTAATCAGTGAGGCGGAGTAAAGAGTCT 963
DB 5386 GTACGCCAGAACTTTGAGAAGTGTATTAATCAGTGAGGCGGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTGTATAGTAATAACATCACTTG 1023
DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTGTATAGTAATAACATCACTTG 5267
QY 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTGCTGTAATATCCAGAACATATTACCGC 1083
DB 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTGCTGTAATATCCAGAACATATTACCGC 5207
QY 1084 CAGCCATTGCACAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 1143
DB 5206 CAGCCATTGCACAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 5147
QY 1144 GAAATGGATTATTACATTTGGCAGATTCCAGCTACACAGCAGTAAATAAAGGGACAT 1203
DB 5146 GAAATGGATTATTACATTTGGCAGATTCCAGCTACACAGCAGTAAATAAAGGGACAT 5087
QY 1204 TCTGGCCACAGAG 1217
DB 5086 TCTGGCCACAGAG 5073

RESULT 14
US-09-727-311-1/c
; Sequence 1, Application US/09727311
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/727,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/767,436
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P31 9072
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ;
 US-09-727-311-1

Query Match 94.6%; Score 1150.8; DB 29; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 ;
 QY 64 ATCATGGTCATAGCTGTTTCCTGTGTAATTTGTTATCGCTCACAATTTCCACACAACAT 123
 DB 6226 ATCTGGTCATAGCTGTTTCCTGTGTAATTTGTTATCGCTCACAATTTCCACACAACAT 6167
 ;
 QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTACACAT 183
 DB 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAGCTAACTACACAT 6107
 ;
 QY 184 AATTGGCTTGGCTCAGTCACGCGCTTTCCAGTCGGAACCTGTCGTCGCCAGCTGCATTA 243
 DB 6106 AATTGGCTTGGCTCAGTCACGCGCTTTCCAGTCGGAACCTGTCGTCGCCAGCTGCATTA 6047
 ;
 QY 244 ATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCTATTGGGCCCAAGGTTGGTTTTC 303
 DB 6046 ATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCTATTGGGCCCAAGGTTGGTTTTC 5987
 ;
 QY 304 TTTTACCAGTGACAGCGGCAAGAGCTGATGGCTTCCAGCGCTGGCCCTGAGAGATT 363
 DB 5986 TTTTACCAGTGACAGCGGCAAGAGCTGATGGCTTCCAGCGCTGGCCCTGAGAGATT 5927
 ;
 QY 364 GCAGCAAGCGTCCAGCTGTTTGGCCCGCAGCGGCAAAATCCTGTTGATGTTGTTTC 423
 DB 5926 GCAGCAAGCGTCCAGCTGTTTGGCCCGCAGCGGCAAAATCCTGTTGATGTTGTTTC 5867
 ;
 QY 424 CGAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTTGT 483
 DB 5866 CGAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTTGT 5807
 ;
 QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGAGCTGAGCTCCAACTCAAGTTCAAGGGCGNAA 543
 DB 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGAGCTGAGCTCCAACTCAAGTTCAAGGGCGNAA 5747
 ;
 QY 544 AACGGTCTATCAGGGCGATGGCCCATACGTGAACCATCAACCCAAATCAAGTTTGGG 603
 DB 5746 AACGGTCTATCAGGGCGATGGCCCATACGTGAACCATCAACCCAAATCAAGTTTGGG 5687
 ;
 QY 604 GTCAGGTGCGGTAAAGCACTAATCGGAACCTTAAGAGGAGCCCCCGATTTAGAGTTG 663
 DB 5686 GTCAGGTGCGGTAAAGCACTAATCGGAACCTTAAGAGGAGCCCCCGATTTAGAGTTG 5627
 ;
 QY 664 ACGGGGAAGCGCGGCAAGCTGGCGAGAGGAAGGAAGGAAGGAAGGAAGGAGCGGCGC 723
 DB 5626 ACGGGGAAGCGCGGCAAGCTGGCGAGAGGAAGGAAGGAAGGAAGGAGCGGCGC 5567
 ;
 QY 724 TAGGGCGTGGCAAGTGTAGCGGTGAGCTGCGGTAAACCAACCAACCCCGCGCTTAA 783
 DB 5566 TAGGGCGTGGCAAGTGTAGCGGTGAGCTGCGGTAAACCAACCAACCCCGCGCTTAA 5507
 ;
 QY 784 TGGCGCGCTACAGGCGCGTACTGTTGCTTTGAGGAGCAGGTATAACGTTGTTTCC 843
 DB 5506 TGGCGCGCTACAGGCGCGTACTGTTGCTTTGAGGAGCAGGTATAACGTTGTTTCC 5447

RESULT 15
 US-09-727-311-5/c
 ; Sequence 5, Application US/09727311
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
 ; TITLE OF INVENTION: RANDOMIZED PEPTIDES
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/727,311
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/767,436
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P31 9072
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ;
 US-09-727-311-5

QY 844 CGTTGGATCAGACCGGGAGCTAAACAGGAGGCGGATTTAAAGGATTTTACAGAGAACG 903
 DB 5446 CGTTGGATCAGACCGGGAGCTAAACAGGAGGCGGATTTAAAGGATTTTACAGAGAACG 5387
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 QY 904 GTACGCCAGAACTCTTGAGAAAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCT 963
 DB 5386 GTACGCCAGAACTCTTGAGAAAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCT 5327
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 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTTG 1023
 DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTTG 5267
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 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGCCTTGGCTGTTAAATATCCAGAACATATTACGC 1083
 DB 5266 CTTGAGTAGAAGAACTCAAACTATCGCCTTGGCTGTTAAATATCCAGAACATATTACGC 5207
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 QY 1084 CAGCCATTGCAACAGGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCTCT 1143
 DB 5206 CAGCCATTGCAACAGGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCTCT 5147
 ;
 QY 1144 GAATGGATTTATACATTGGCAGATTCCACAGTCCACAGCAGTAAATAAAGGGACAT 1203
 DB 5146 GAATGGATTTATACATTGGCAGATTCCACAGTCCACAGCAGTAAATAAAGGGACAT 5087
 ;
 QY 1204 TCTGGCCAAACAGAG 1217
 DB 5086 TCTGGCCAAACAGAG 5073

Query Match				94.6%;	Score 1150.8;	DB 29;	Length 7294;				
Best Local Similarity				99.8%;	Pred. No. 0;						
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Qy	124	ACGAGCCGGAAGCAATAAAGTGTAAAGCTTGGGGTGCCTTAATGAGTGAGCTAACTCAACAT	183								
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Qy	184	AAATGCGCTTGGCTCACTGCGCCGCTTCCAGTCGGGAAACCTGCTGCGCCAGCTGCATTA	243								
Db	6106	AAATGCGCTTGGCTCACTGCGCCGCTTCCAGTCGGGAAACCTGCTGCGCCAGCTGCATTA	6047								
Qy	244	ATGAATCGGCAACGCGCGGGAGAGCGGTTCGCTAATTCGGGCGCCAGGGTGGTTC	303								
Db	6046	ATGAATCGGCAACGCGCGGGAGAGCGGTTCGCTAATTCGGGCGCCAGGGTGGTTC	5987								
Qy	304	TTTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCACCGCTGGGCCCTGAGAGATT	363								
Db	5986	TTTTTCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCACCGCTGGGCCCTGAGAGATT	5927								
Qy	364	GCAGCAAGCGTCCACGCTGCTTTGCCCGCAGCAGCGAAATCCCTGTTTGTATGTTGTTTC	423								
Db	5926	GCAGCAAGCGTCCACGCTGCTTTGCCCGCAGCAGCGAAATCCCTGTTTGTATGTTGTTTC	5867								
Qy	424	CGAAATCGGCAAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGGTTGAGTGTGT	483								
Db	5866	CGAAATCGGCAAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGGTTGAGTGTGT	5807								
Qy	484	TCCAGTTTGGCAACAGAGTCCACTATTAAGAAAGCTGGACTCCACCTCAAGGGCGGAA	543								
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Qy	544	AACGCTCTATCAGGGCGATGCCCTACTACTGAAACCTACCCCAATCAAGTTTTTTGGG	603								
Db	5746	AACGCTCTATCAGGGCGATGCCCTACTACTGAAACCTACCCCAATCAAGTTTTTTGGG	5687								
Qy	604	GTGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCCCGGATTTAGAGCTTG	663								
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Qy	664	ACGGGGAAGCGCGGAGCTGGCGAGAAAGGAGGAAAGGAGGAGGAGGCGC	723								
Db	5626	ACGGGGAAGCGCGGAGCTGGCGAGAAAGGAGGAAAGGAGGAGGAGGCGC	5567								
Qy	724	TAGGGCGCTGGCAAGTGTAGCGGTGACGCTGCGGTAAACACACACCCCGCGCTTAA	783								
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Qy	784	TGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGGTATACGTGCTTTCCT	843								
Db	5506	TGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGGTATACGTGCTTTCCT	5447								
Qy	844	CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGCGATTAAGGGATTTTAGACAGGAACG	903								
Db	5446	CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGCGATTAAGGGATTTTAGACAGGAACG	5387								
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Db	5386	GTACGCCAGAATCTTGAGAGTGTATTAATATCAGTGAAGGCCACCGAGTAAAGAGTCT	5327								
Qy	964	GTCCATACGCCAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAAATACATCACTTG	1023								
Db	5326	GTCCATACGCCAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAAATACATCACTTG	5267								
Qy	1024	CTGAGTGAAGAATCAAACTATCCGCTTGTGCTGCTAATATCCAGAACAAATATTACCGC	1083								
Db	5266	CTGAGTGAAGAATCAAACTATCCGCTTGTGCTGCTAATATCCAGAACAAATATTACCGC	5207								
Qy	1084	CAGCCATTGCAACAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCTCT	1143								

Db	5206	CAGCCATTGCAACAGGAAACCGCTCATGGAATAACCTACATTTTGACGCTCAATCGTCT	5147
Qy	1144	GAATGGATTATTTACATTTGGCAGATTCCACAGTCACAGCAGTAATAAAGGACAT	1203
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Qy	1204	TCTGGCCCAACAGAG	1217
Db	5086	TCTGGCCCAACAGAG	5073

Search completed: August 1, 2002, 10:59:18
Job time: 11349 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 08:40:05 ; Search time 348.01 Seconds
(without alignments)
7578.543 Million cell updates/sec

Title: US-10-014-743-1
Sequence: 1 GCCAGCTTCATGCTGCA.....GGACATTCGCCAACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1353370 seqs, 1083569762 residues

Total number of hits satisfying chosen parameters: 2706740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New.*
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2: /cgn2_6/ptodata/1/pna/US05_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
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8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	931.2	76.5	9532	1	PCT-US02-12405-451
C 2	931.2	76.5	9532	7	US-10-045-674-451
C 3	928	76.3	10251	1	PCT-US02-12405-582
C 4	928	76.3	10251	7	US-10-045-674-582
5	592.6	48.7	605	5	US-09-334-818A-4
6	592.6	48.7	605	5	US-09-334-818A-23
7	590.4	48.5	601	5	US-09-334-818A-19
8	581	47.7	604	5	US-09-334-818A-24
9	577.4	47.4	605	5	US-09-334-818A-17
10	574.4	47.2	605	5	US-09-334-818A-12
11	574	47.2	598	5	US-09-334-818A-11
12	572.4	47.0	602	5	US-09-334-818A-22
13	564	46.3	601	5	US-09-334-818A-18
14	558.8	45.9	595	5	US-09-334-818A-5
15	551.4	45.3	605	5	US-09-334-818A-21
16	551	45.3	596	5	US-09-334-818A-13
17	551	45.3	597	5	US-09-334-818A-10
18	526.6	43.3	599	5	US-09-334-818A-6
19	505.8	41.6	591	5	US-09-334-818A-3
20	488	40.1	619	5	US-09-334-818A-20
21	459.8	37.8	597	5	US-09-334-818A-16
22	445.2	36.6	602	5	US-09-334-818A-14
C 23	432.4	35.5	4455	7	US-10-047-542-13
C 24	432.4	35.5	6602	7	US-10-047-542-100
25	432.4	35.5	7129	7	US-10-047-542-101

Sequence 14, Appl
Sequence 7, Appl
Sequence 522, App
Sequence 522, App
Sequence 1, Appl
Sequence 53, Appl
Sequence 15, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 75, Appl
Sequence 9, Appl
Sequence 46, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 32, Appl
Sequence 40, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 35, Appl

26 432.4 35.5 8074 7 US-10-047-542-14
27 426 35.0 585 5 US-09-334-818A-7
28 399.4 32.8 6880 1 PCT-US02-12405-522
29 399.4 32.8 6880 7 US-10-045-674-522
C 30 399 32.8 4026 5 US-09-949-039-1
C 31 399 32.8 10325 7 US-10-112-267-53
32 395.2 32.5 602 5 US-09-334-818A-15
33 381.2 31.3 8157 7 US-10-038-722-70
34 381.2 31.3 8584 7 US-10-038-722-71
35 381.2 31.3 8590 7 US-10-038-722-75
C 36 379.6 31.2 652 5 US-09-570-582C-9
37 379.6 31.2 2989 7 US-10-149-736-46
C 38 379.6 31.2 4570 7 US-10-049-404-1
39 379.6 31.2 4704 5 US-09-932-328-4
40 379.6 31.2 4727 5 US-09-756-577-16
C 41 379.6 31.2 4773 5 US-09-991-209-32
C 42 379.6 31.2 4847 5 US-09-756-577-40
C 43 379.6 31.2 4950 5 US-09-991-209-34
C 44 379.6 31.2 4965 5 US-09-991-209-37
C 45 379.6 31.2 4974 5 US-09-991-209-35

ALIGNMENTS

RESULT 1
PCT-US02-12405-451/c
Sequence 451, Application PC/TUS0212405

GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: PCT/US02/12405
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 451
LENGTH: 9532
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3 nucleotide
OTHER INFORMATION: sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1579)..(1638)
FEATURE:
NAME/KEY: CDS
LOCATION: (2343)..(3443)
FEATURE:
NAME/KEY: CDS
LOCATION: (3945)..(4400)
FEATURE:
NAME/KEY: CDS
LOCATION: (4406)..(4450)
FEATURE:
NAME/KEY: CDS
LOCATION: (4746)..(5789)
PCT-US02-12405-451

Query Match				76.5%;	Score 931.2;	DB 1;	Length 9532;
Best Local Similarity				97.6%;	Pred. No. 3.3e-256;		
Matches 945;				Conservative	0;	Mismatches 23;	Indels 0;
				Gaps			
QY	250	CGGCCAACGCGCGGGGAGAGCGGTATGGCGTATTTGGCGCGCACGGGTGGTTTTCTTTTCA	309				
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QY	310	CCAGTGAGAGCGGCAACAGCTGATGGCCCTTCACGGCTCGCCCTGAGAGAGTTGCGACGA	369				
DB	7531	CCAGTGAGAGCGGCAACAGCTGATGGCCCTTCACGGCTCGCCCTGAGAGAGTTGCGACGA	7472				
QY	370	AGCGGTCCACGCTGGTTTGGCCGACAGCGGAAATCCTGTTGATGGTGGTCTCCGAAT	429				
DB	7471	AGCGGTCCACGCTGGTTTGGCCGACAGCGGAAATCCTGTTGATGGTGGTCTCCGAAT	7412				
QY	430	CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTCTGTTCCAGT	489				
DB	7411	CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTCTGTTCCAGT	7352				
QY	490	TTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGTCAAAAGGGCGAAAAACCGT	549				
DB	7351	TTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGTCAAAAGGGCGAAAAACCGT	7292				
QY	550	CTATCAGGGCGATGGCCCACTAGTGAACCATCACCCAAATCAAGTTTTTGGGGTCGAG	609				
DB	7291	CTATCAGGGCGATGGCCCACTAGTGAACCATCACCCAAATCAAGTTTTTGGGGTCGAG	7232				
QY	610	GTGCGTAAAGCACTAAATCGAAACCTTAAGGGAGCCCGCAATTTAGAGCTTTGACGGGG	669				
DB	7231	GTGCGTAAAGCACTAAATCGAAACCTTAAGGGAGCCCGCAATTTAGAGCTTTGACGGGG	7172				
QY	670	RAAGCCGGCAACGTGGCGAGAAAGGAAGGAAAGCAAGAGCGGGCGCTAGGGC	729				
DB	7171	RAAGCCGGCAACGTGGCGAGAAAGGAAGGAAAGCAAGAGCGGGCGCTAGGGC	7112				
QY	730	GCTGCAAGTGTAGCGGTCAACGCTGCGCTTAACCAACCGCCGCGCTTAATCGGC	789				
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QY	790	GCTACAGGGCGGTACTATGGTTGTTTACGAGCACGCTATAACGTGCTTTCTCGTTGG	849				
DB	7051	GCTACAGGGCGGTACTATGGTTGTTTACGAGCACGCTATAACGTGCTTTCTCGTTGG	6992				
QY	850	AATCAGACGGGAGCTAAACAGAGCGCGATTAAAGGGATTTAGACAGAACCGGTACGC	909				
DB	6991	AATCAGACGGGAGCTAAACAGAGCGCGATTAAAGGGATTTAGACAGAACCGGTACGC	6932				
QY	910	CAGAACTTGAGAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCTGTGCCAT	969				
DB	6931	CAGAACTTGAGAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCTGTGCCAT	6872				
QY	970	CACCAAAATTAACCGTTCTAGCAATACCTTTGATTAGTATATACATCATTCGCTGAG	1029				
DB	6871	CACCAAAATTAACCGTTCTAGCAATACCTTTGATTAGTATATACATCATTCGCTGAG	6812				
QY	1030	TAGAAGAACTCAAACTATCGGCCCTTGCTGGTAATATCCAGAAACAATATTACGCCAGCCA	1089				
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QY	1090	TTGCAACAGGAAAACCGTCAATGGAATACTTACATTTTGACGCTCAATCGTCTGAAATG	1149				
DB	6751	TTGCAACAGGAAAACCGTCAATGGAATACTTACATTTTGACGCTCAATCGTCTGAAATG	6692				
QY	1150	GATTATTATACATTGGCAGATTCACAGTCACAGCACGACAGTATATAAGGGACATTTCTGC	1209				
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QY	1210	CAACAGAG 1217					
DB	6631	CAACAGAG 6624					

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RESULT      2
US-10-045-674-451/c
; Sequence 451, Application US/10045674
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9532
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALLIA3 nucleotide
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1579)..(1638)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2343)..(3443)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3945)..(4400)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4406)..(4450)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4746)..(5789)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4746)..(5789)
; US-10-045-674-451

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[illegible]

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CJRA05
; OTHER INFORMATION: nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1578)..(1916)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2388)..(2843)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2849)..(2893)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3189)..(4232)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7418)..(8119)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8160)..(9452)
; PCT-US02-12405-582

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Query Match 76.3% Score 928; DB 1; Length 10251;
Best Local Similarity 97.4%; Pred. No. 2.8e-255;
Matches 943; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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DB 6034 CGCATATTTCCCGGAAAGTGCACCTGGATGTCAGGGTGGTTTCTTTTCA 5975
QY 310 CCAGTGAGAGGGGAAAGAGTGTGGCTTTCACGGCTGGCTTTCAGAGAGTTGCACCA 369
DB 5974 CCAGTGAGAGGGGAAAGAGTGTGGCTTTCACGGCTGGCTTTCAGAGAGTTGCACCA 5915
QY 370 AGCGGTCCAGCTGTTTGGCCCGAGAGGCGGAAATCTGTTGATGGTGGTCCGAAAT 429
DB 5914 AGCGGTCCAGCTGTTTGGCCCGAGAGGCGGAAATCTGTTGATGGTGGTCCGAAAT 5855
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DB 5854 CGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTCAGTGTGTTCCAGT 5795
QY 490 TTGGAACAAGAGTCCACTATTAAAGACGTGACCTCCACGTCACCAAGGCGGAAACCGT 549
DB 5794 TTGGAACAAGAGTCCACTATTAAAGACGTGACCTCCACGTCACCAAGGCGGAAACCGT 5735
QY 550 CTATCAGGGCGATGCCCGACTACGTGAACCATCACCCAAATCAAGTTTTTGGGGTCGAG 609
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DB 5674 GTGCCGTAAAGCACTAAATCGGAACCTTAAGGGAGAGCCCGGATTTAGAGCTTGACGGGG 5615
QY 670 AAAGCCGCGAAGCTGGCGGAGAAAGGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGG 729
DB 5614 AAAGCCGCGAAGCTGGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5555
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QY 790 GCTACAGGGCGGTACTATGTTGTTTACGAGGACGATATACGTCGTTCTCGTTGG 849
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QY 850 AATCAGAGGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTAGACAGGAGGAGGAGG 909
DB 5434 AATCAGAGGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTAGACAGGAGGAGGAGG 5375

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RESULT . 3
PCT-US02-12405-582/c
; Sequence 582. Application PC/TUS0212405
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOENENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: PCT/US02/12405
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 06/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10251

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Db 5374 CAGATCTTGAGAACTGTTTATATATACAGTGAGGCCACCGAGTAAAGAGTCTGTCCAT 5315
QY 970 CACGCAAAATTAACCGTGTAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 1029
Db 5314 CACGCAAAATTAACCGTGTAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 5255
QY 1030 TAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACTATATACCGCCAGCCA 1089
Db 5254 TAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACTATATACCGCCAGCCA 5195
QY 1090 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATGCTGAAATG 1149
Db 5194 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATGCTGAAATG 5135
QY 1150 GATTATTTACATTTGCCAGATTCACCAAGTACACAGCAGTACAGACAGTATATAAAGGACATTCCTGGC 1209
Db 5134 GATTATTTACATTTGCCAGATTCACCAAGTACACAGCAGTACAGACAGTATATAAAGGACATTCCTGGC 5075
QY 1210 CAACAGAG 1217
Db 5074 CAACAGAG 5067

RESULT 4
US-10-045-674-582/c
; Sequence 582, Application US/10045674
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045.674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 05/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CJRA05
; OTHER INFORMATION: nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1578)..(1916)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2388)..(2843)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2849)..(2893)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3189)..(4232)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7418)..(8119)
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (8160)..(9452)
us-10-045-674-582
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Query Match 76.3%; Score 928; DB 7; Length 10251;
Best Local Similarity 97.4%; Pred. No. 2.8e-255;
Matches 943; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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QY 250 CGGCCAACCCGCGGGGAGAGCGGTTTGGCGCTATTGGCGCGCAGGCTGTTTTCTTTTCA 309
Db 6034 CGCACATTTCCCGAAGAGTGCCACCTGCAAGCTTGGATCCAGGGTGGTTTTCTTTTCA 5975
QY 310 CAGTGAGACGGGCAACAGCTGATTCGCCCTTACCGCTGCGCCCTGAGAGAGTTGCAGCA 369
Db 5974 CAGTGAGACGGGCAACAGCTGATTCGCCCTTACCGCTGCGCCCTGAGAGAGTTGCAGCA 5915
QY 370 AGCGCTCCACGCTGTTTGGCCCGCAGCAGGCGAATACTCTTTGATGATGGTTCGGAAT 429
Db 5914 AGCGCTCCACGCTGTTTGGCCCGCAGCAGGCGAATACTCTTTGATGATGGTTCGGAAT 5855
QY 430 CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGT 489
Db 5854 CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGT 5795
QY 490 TTGGAACAAGAGTCCCACTATTAAAGAACGTTGGACTCCAACGTCAAGGGCGAAGACCGT 549
Db 5794 TTGGAACAAGAGTCCCACTATTAAAGAACGTTGGACTCCAACGTCAAGGGCGAAGACCGT 5735
QY 550 CTATCAGGCGGATGCGCCACTACGTGAACCATCACCAAAATCAAGTTTTTGGGCTCGAG 609
Db 5734 CTATCAGGCGGATGCGCCACTACGTGAACCATCACCAAAATCAAGTTTTTGGGCTCGAG 5675
QY 610 GTGCCGTAAGACACTAAATCGGAACCTAAAGGGAGCCCGCGATTTAGAGCTTCACGGG 669
Db 5674 GTGCCGTAAGACACTAAATCGGAACCTAAAGGGAGCCCGCGATTTAGAGCTTCACGGG 5615
QY 670 AAAGCGCGCAACGTTGGCGAGAAAGAGGAAAGCAAGAGAGCGGCGCTAGGCG 729
Db 5614 AAAGCGCGCAACGTTGGCGAGAAAGAGGAAAGCAAGAGAGCGGCGCTAGGCG 5555
QY 730 GCTGCAAGTGTAGCGGTACGCTGCGCTAACACACACCGCCGCTTAATGGCC 789
Db 5554 GCTGCAAGTGTAGCGGTACGCTGCGCTAACACACACCGCCGCTTAATGGCC 5495
QY 790 GCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATACGCTCTTCCTCGTTG 849
Db 5494 GCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATACGCTCTTCCTCGTTG 5435
QY 850 AATCAGACCGGAGCTAAACAGGAGCGCGATTAAGGGATTTTAGACAGAAACGCTACGC 909
Db 5434 AATCAGACCGGAGCTAAACAGGAGCGCGATTTAAAGGGATTTTAGACAGAAACGCTACGC 5375
QY 910 CAGAACTTTGAGAACTGTTTTTATATCAGTGAGGCCACCGAGTAAAGAGTCTGTCCAT 969
Db 5374 CAGAACTTTGAGAACTGTTTTTATATCAGTGAGGCCACCGAGTAAAGAGTCTGTCCAT 5315
QY 970 CACGCAAAATTAACCGTGTAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 1029
Db 5314 CACGCAAAATTAACCGTGTAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 5255
QY 1030 TAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACTATATACCGCCAGCCA 1089
Db 5254 TAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACTATATACCGCCAGCCA 5195
QY 1090 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATGCTGAAATG 1149
Db 5194 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATGCTGAAATG 5135
QY 1150 GATTATTTACATTTGCCAGATTCACCAAGTACACAGCAGTACAGACAGTATATAAAGGACATTCCTGGC 1209
Db 5134 GATTATTTACATTTGCCAGATTCACCAAGTACACAGCAGTACAGACAGTATATAAAGGACATTCCTGGC 5075
QY 1210 CAACAGAG 1217
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QY 481 TGTTCAGTTGGACACAGAGTCCACTATTAAAGAACGTTGGACTCCAAAGTCAAAGGGCG 540
 |||||
 Db 492 tttccagcttggaaacaagantccactattaaagaacgtggactccaacgtcaaaaggcg 551
 |||||
 QY 541 AAAAACCGTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCACCAATCAAG 594
 |||||
 Db 552 aaaaacgtctatcagggcgatggcccaactcgtgaaccatcaccccaatcaas 605
 |||||

RESULT 7
 US-09-334-818A-19
 ; Sequence 19, Application US/09334818A
 ; GENERAL INFORMATION:
 ; APPLICANT: DAVIS, MARIA
 ; APPLICANT: FULLER, CARL W.
 ; APPLICANT: MAMONE, JOSEPH A.
 ; APPLICANT: HUANG, LIN
 ; TITLE OF INVENTION: FY7 POLYMERASE
 ; FILE REFERENCE: PB9817
 ; CURRENT APPLICATION NUMBER: US/09/334,818A
 ; CURRENT FILING DATE: 1999-06-17
 ; PRIOR APPLICATION NUMBER: 60/089,556
 ; PRIOR FILING DATE: 1998-06-17
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 19
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Thermus sp.
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (2)
 ; OTHER INFORMATION: a, t, c or g
 ; NAME/KEY: modified_base
 ; LOCATION: (580)
 ; OTHER INFORMATION: a, t, c or g
 US-09-334-818A-19

Query Match 48.5%; Score 590.4; DB 5; Length 601;
 Best Local Similarity 99.7%; Pred. No. 5.7e-159;
 Matches 591; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCAAGCTTGATGCTGCTGAGGTGCACTTAGAGGATCCCGGATCCCGGATCCAGAGTCGCAATTCG 61
 |||||
 Db 9 ccgagcttgatgctgctgaggtcgactctagaggtcccggtaccgagctcgaaatcg 68
 |||||
 QY 62 TAATCATGGTCATAGCTGTTCCCTGTGTGAATTTGTAATTCGCTCACAATTCACACAAAC 121
 |||||
 Db 69 taatcatggtcatagctgttccctgtgtgaattgttatccgctcaccaattccacacac 128
 |||||
 QY 122 ATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTCAGCTAACTCACA 181
 |||||
 Db 129 atcagagccgaagcataaaagttaaagcctggggtgcctaatgagtgagctaacacaca 188
 |||||
 QY 182 TTAATTCGTTGCGCTCACTGCCGCTTCCAGTCGGGAACCTGTGCTGCCAGCTGCAT 241
 |||||
 Db 189 ttaattgcttgctcactgcgcgcttccagtcgggaacacctgtcgtgcagctgcat 248
 |||||
 QY 242 TAATGAATCGCCCAACCGCGGGGAGAGCGGTTTGGCTATTGGCGCCAGGTTGTTT 301
 |||||
 Db 249 taatgaatcgcccaacgcgcggagagcggttctcgtatcgggcccagggtggtttt 308
 |||||
 QY 302 TCCTTTCCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGAG 361
 |||||
 Db 309 tctttccacagtgagacgggcaacagctgattgcccctcacgcctggccctgagagag 368
 |||||
 QY 362 TTGCAGCAAGCGGTCCACGCTGTTGGCCCGACGCGGAAATTCCTGTTGATGGTGG 421
 |||||
 Db 369 ttgcagcaagcggtccacgctggtttggcccccagcagcgcaaaatcctgtttgatggtg 428
 |||||

QY 422 TCCGAATCGGCAAAATCCCTTTATAATCAAAAGAAATAGCCGAGATAGGCTTGAGTGT 481
 |||||
 Db 429 tccgaatcgcgcaaaatcccttataataatcaaaagataagccgagatagg99ttgagtt 488
 |||||
 QY 482 GTTCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTTGGACTCCAAAGTCAAAGGGCGA 541
 |||||
 Db 489 gttccagtttggaaacaagagtcactattaaagaacgtggactccaacgtcaaaaggcg 548
 |||||
 QY 542 AAAACCGTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCACCAATCAAG 594
 |||||
 Db 549 aaaaacgtctatcagggcgatggcccaactcactgaaccatcaccccaatcaag 601
 |||||

RESULT 8
 US-09-334-818A-24
 ; Sequence 24, Application US/09334818A
 ; GENERAL INFORMATION:
 ; APPLICANT: DAVIS, MARIA
 ; APPLICANT: FULLER, CARL W.
 ; APPLICANT: MAMONE, JOSEPH A.
 ; APPLICANT: HUANG, LIN
 ; TITLE OF INVENTION: FY7 POLYMERASE
 ; FILE REFERENCE: PB9817
 ; CURRENT APPLICATION NUMBER: US/09/334,818A
 ; CURRENT FILING DATE: 1999-06-17
 ; PRIOR APPLICATION NUMBER: 60/089,556
 ; PRIOR FILING DATE: 1998-06-17
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 604
 ; TYPE: DNA
 ; ORGANISM: Thermus sp.
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (512)
 ; OTHER INFORMATION: a, t, c or g
 US-09-334-818A-24

Query Match 47.7%; Score 581; DB 5; Length 604;
 Best Local Similarity 99.7%; Pred. No. 2.8e-156;
 Matches 592; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAAGCTTGCAATGCTGCGAGTCCGACTTAGAGGATCCCGGATCCCGGATCCAGCTCGAATTC 60
 |||||
 Db 12 gccaaagcttgcaatgctgctgaggtcgactctagaggtcccggtaccgagctcgaaattc 71
 |||||
 QY 61 GTAATCATGTCATAGCTGTTCCCTGTGTGAATTTGTTATCCGCTCACAATTCACACAA 120
 |||||
 Db 72 gcaatcatggtcatagctgttccctgtgtgaattgttatccgctcaccaattccacacaa 131
 |||||
 QY 121 CATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTCAGCTAACTCAC 180
 |||||
 Db 132 catcagagccggaagcataaaagttaaagcctggggtgcctaatgagtgagctaacctac 191
 |||||
 QY 181 ATTAATTCGTTGCGCTCACTGCCGCTTCCAGTCGGGAACCTGTGCTGCCAGCTGCA 240
 |||||
 Db 192 attaattgcttgctcactgcgcgcttccagtcgggaacacctgtcgtgcagctgca 251
 |||||
 QY 241 TTAATGAATCGCCCAACCGCGGGGAGAGCGGTTTGGCTATTGGCGCCAGGTTGTTT 300
 |||||
 Db 252 ttaatgaatcgcccaacgcgcggagagcggttctcgtatcgggcccagggtggtttt 311
 |||||
 QY 301 TTCCTTTCCACAGTGAGACGGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGA 360
 |||||
 Db 312 tctttccacagtgagacgggcaacagctgattgcccctcacgcctggccctgagagag 371
 |||||
 QY 361 GTTCAGCAAGCGGTCCACGCTGTTGGCCCGACGCGGAAATTCCTGTTGATGGTGG 420
 |||||
 Db 372 ttgcagcaagcggtccacgctggtttggcccccagcagcgcaaaatcctgtttgatggtg 431
 |||||
 QY 421 TCCGAATCGGCAAAATCCCTTTATAATCAAAAGAAATAGCCGAGATAGGCTTGAGTGT 480
 |||||

Db 317 tcaccagtgagagcgagcgagcctgctgctccctccgagagaggttga 376
QY 367 GCAAGCGGTCCACGCTGGTTGGCCAGAGCGGAAATCCTGTTGATGCTGTTCCGA 426
Db 377 gcaagcggtccacgctggttggcccgagcgaggaatcctgttggatggtggtccga 436
QY 427 AATCGGCAAAATCCCTTATTAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTGTTCC 486
Db 437 aatcggaataatcccttataatacaaaagaaatagcccgagataggttggatggttcc 496
QY 487 AGTTTGGAAACAGAGTCCACTATTAAGAAAGAGCTGCAAGCTCAAAAGGCGGAAATAC 546
Db 497 agtttggaaacaagantccactattaaagaacgtggaactccaaacgctcaaaagggcgaaaaac 556
QY 547 CTTCTATCAGGCGATGCGCCACTACGTGAACCATCATCCCAATCAAGT 595
Db 557 cgtctatcagggcggaagggccactacntgaaccatcccaaatcaagt 605

RESULT 10
US-09-334-818A-12
; Sequence 12 Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FV7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2)..(12)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (27)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (523)
; OTHER INFORMATION: a, t, c or g
; US-09-334-818A-12

Query Match 47.2%; Score 574.4; DB 5; Length 605;
Best Local Similarity 99.7%; Pred. No. 2.e-154;
Matches 575; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTTGATGCTGCAGTGCAGTCTAGAGATCCCGGGTACCGAGCTCGAATTCGTAATC 66
Db 29 ctgcatgctgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 88
QY 67 ATGGTCATAGCTGTTTCCTGTTGAAATGTTATCGCTCACAATTCACACAAATACG 126
Db 89 atggtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 148
QY 127 AGCCGGAACATTAAGTGAAGCTGCTTAATGAGTGAGTAACTACATTAAT 186
Db 149 agccggaagcataaagtgtaaagccctggggtgcttaagtgagtaactcacataat 208
QY 187 TGCGTTGCGTCACTCGCGCTTTCCAGTCGGGAAACCTGTCGTCGACCTGCAATTAATG 246
Db 209 tgcgttgcctcactgcccgttcttcgagtcgggaaacctgtcgtgcccagctgcatatg 268

Db 432 ttccgaatcgcaaatccctataataatcaaaagataagcccgagagaggttgagtg 491
QY 481 TGTTCCTAGTTTGGAAAGAGTCCACTATTAAAGAAAGTGGAGTCCCAAGCTCAAAAGGCG 540
Db 492 tgttcagcttgggaacaagantccactattaaagaagtggaactccaacgccaagggcg 551
QY 541 AAAAACCTCTATCAGGCGGATGCGCCACTACGTGAACCATCACCCCAATCAAG 594
Db 552 aaaaa-cgtctatcagggcgatggccactacgtgaaccatccacccaatcaag 604

RESULT 9
US-09-334-818A-17
; Sequence 17 Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FV7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (16)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (511)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (583)
; OTHER INFORMATION: a, t, c or g
; US-09-334-818A-17

Query Match 47.4%; Score 577.4; DB 5; Length 605;
Best Local Similarity 98.6%; Pred. No. 3.e-155;
Matches 581; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 7 CTTGATGCTGCAGTGCAGTCTAGAGATCCCGGGTACCGAGCTCGAATTCGTAATC 66
Db 17 ctgcatgctgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 76
QY 67 ATGGTCATAGCTGTTTCCTGTTGAAATGTTATCGCTCACAATTCACACAAATACG 126
Db 77 atggtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 136
QY 127 AGCCGGAACATTAAGTGAAGCTGCTTAATGAGTGAGTAACTACATTAAT 186
Db 137 agccggaagcataaagtgtaaagccctggggtgcttaagtgagtaactcacataat 196
QY 187 TGCGTTGCGTCACTCGCGCTTTCCAGTCGGGAAACCTGTCGTCGACCTGCAATTAATG 246
Db 197 tgcgttgcctcactgcccgttcttcgagtcgggaaacctgtcgtgcccagctgcatatg 256
QY 247 AATCGGCAACGCGCGGGAGAGCGGTTTGCCTATTGGCGCCAGGCTGTTTCTTT 306
Db 257 aatcggaacagcgcggggagagcggtttcgatggcgccaggggtgtttcttt 316
QY 307 TCACCACTGAGAGCGGGCAACAGCTGATTGCTTCACCGCTGCGCCCTGAGAGAGTTGCA 366

QY 247 AATCGCCACACGCGGGGAGAGCGGTTTTCGTAATTTGGCGCCAGGCTGTTTCTTT 306
Db 269 aatcgccacacgcgcgggagagcggtttcgattggcgccaggggtggtttctttt 328
QY 307 TCACCAAGTGCAGCGGCAACAGCTGATTCGCCCTTACCGGCTGGCCCTGAGAGAGTTGCA 366
Db 329 tcaccagtgagagcgagcgagcgtgattgcccctcccgccctggccctgagagagttgca 388
QY 367 GCAAGCGGTTCACGCTGCTTCCCGCAGAGCGGCAAAATCCCTTTGATGGTGGTTCGGA 426
Db 389 gcaagcggtccacgcgtggtttgcccacagcagcgagaaatccctggttgaagggttccga 448
QY 427 AATCGCAAAATCCCTTATAATCAAAAGAGATAGCCCGAGATAGGTTGAGTGTTCCTCC 486
Db 449 aatcgcaaaatcccttataatcaaaagagatagcccgagataggtttgagttgttcc 508
QY 487 AGTTTGGACAGAGTCCCACTATTAAAGAACGTGGACTCCAAAGTCGAAGGCGGAAAC 546
Db 509 agtttggacagagantccactattaaagacgtggactcccaacgccaagggcgaaaaac 568
QY 547 CGTCTATCAGGCGGATGCCCGCACTACGTGAACCATCA 583
Db 569 cgtctacagggcgatggcccaactacgtgaaccatca 605

RESULT 11

US-09-334-818A-11

; Sequence 11, Application US/09334818A

; GENERAL INFORMATION:

; APPLICANT: DAVIS, MARIA

; APPLICANT: FULLER, CARL W.

; APPLICANT: MAMONE, JOSEPH A.

; APPLICANT: HUANG, LIN

; FILE REFERENCE: PB9817

; CURRENT APPLICATION NUMBER: US/09/334,818A

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: 60/089,556

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 598

; TYPE: DNA

; ORGANISM: Thermus sp.

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (1)

; OTHER INFORMATION: a, t, c or g

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (15)

; OTHER INFORMATION: a, t, c or g

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (512)

; OTHER INFORMATION: a, t, c or g

; US-09-334-818A-11

Query Match

Best Local Similarity 47.2%; Score 574; DB 5; Length 598;

Matches 585; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCCAAGCTTCATGCTCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
Db 12 gccnagcttcgactgcgaggtcgactctagagatcccggttacccgagctcgaaattc 71
QY 61 GTAATCATGTCATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCAAAATTCACACAA 120
Db 72 gtaatcatggtcatagctgctttctctgtgtgaaattgttaccgttccattccacaaa 131

QY 121 CATACGAGCCGGAACATATAAGTGTAAAGCCTGGGGTGCCTTAATGAGTACGTAACCTAC 180
Db 132 catacgagccggaagcataaagtgtaagcctggggtgcttaagtgagtgagtaactcac 191
QY 181 ATTAATTTGGCTTGGCTGCTACATGCGCCGCTTTCAGTTCGGGAAACCTGTGTCGACGCTGCA 240
Db 192 attaattgctgtgctgctcactgcccgtttccagtcgggaaacctgtcgtgccagctgca 251
QY 241 TTAATGAATCGCCCAACGCGGGAGAGCGGTTTGGGTATTTGGGCCGCCAGGTTGTTT 300
Db 252 ttaatgaatcgcccaacgcgcggggagagcggtttcgattgggcccaggggtggttt 311
QY 301 TTCTTTTCCACAGTGCAGCGGCAACAGCTGATTGCCCTTTCACCGCTGGCCCTGAGAGA 360
Db 312 ttcttttccacagtgagacgggcaacagctgattgcccctcaccgcctggcccctgagaga 371
QY 361 GTTGACGAGCAAGCGTCCACGCTGTTTGGCCCCAGCAGCGGAAATCTGTTGATGGTGG 420
Db 372 gttgcagcaagcgttccacgctggtttgcccagcagggcgaaaatcctgttggatggtg 431
QY 421 TTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 480
Db 432 ttccgaaatcggaataatcccttataaatacaaaagataagcccgagataggtggtgt 491
QY 481 TGTTCCAGTTTGAACAGAGTCCACTATTAAAGAACGTGGACTCCCAACGTCGAAGGCGG 540
Db 492 gttccagtttggaaacaagantccactattaaagacgtggactcccaacgtcaaaagcg 551
QY 541 AAAAAACGTTCTATCAGGCGGATGGCCCACTAGCTGAACCATCACCCAA 588
Db 552 aaaaa-cgtctatcagggcgatggcccaactacgtgaaccatcacccaa 598

RESULT 12

US-09-334-818A-22

; Sequence 22, Application US/09334818A

; GENERAL INFORMATION:

; APPLICANT: DAVIS, MARIA

; APPLICANT: FULLER, CARL W.

; APPLICANT: MAMONE, JOSEPH A.

; APPLICANT: HUANG, LIN

; TITLE OF INVENTION: FY7 POLYMERASE

; FILE REFERENCE: PB9817

; CURRENT APPLICATION NUMBER: US/09/334,818A

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: 60/089,556

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 602

; TYPE: DNA

; ORGANISM: Thermus sp.

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (2)

; OTHER INFORMATION: a, t, c or g

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (569)

; OTHER INFORMATION: a, t, c or g

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (585)

; OTHER INFORMATION: a, t, c or g

; US-09-334-818A-22

Query Match

Best Local Similarity 47.0%; Score 572.4; DB 5; Length 602;

Matches 584; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCCAAGCTTCATGCTCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60

us-10-014-743-1.rnnp

Thu Aug 1 12:08:41 2002

NAME/KEY: modified_base
LOCATION: (16)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (405)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (512)
OTHER INFORMATION: a, t, c or g
US-09-334-818A-18

Query Match 46.3%; Score 564; DB 5; Length 601;
Best Local Similarity 99.0%; Pred. No. 2.1e-151;
Matches 586; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GCCAAGCTTCATGCC -TGCAGGTCGACTCTAGAGATCCCCGGGTACCGAGCTCGAATT 59
Db 11 gccnacttgcagcttgcaggtcgcactctagagatccccgggtacccagagctgaatt 70
QY 60 CGTAATCATGGTCATAGCTGTTTCTCTGTGAAATTGTTATCCGCTCACAAATTCACACA 119
Db 71 cgtaatcatggtcatagctgttctctgtgaaattgtatccgctcacattccacaca 130
QY 120 ACATACGAGCGGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGATGAGTGAAGTCA 179
Db 131 acatacagcgcggaagcataaagtgtaaagcctgggtgcttaataatgagtgagtaactca 190
QY 180 CATTAATTCGCTGGCTCACTGCGGCTTCCAGTTCGGGAAACCTGTCGTCGAGCTGC 239
Db 191 cattaattgcgttgcgtcactgcgcgttccagtcgggaacctgtcgtgcccagctgc 250
QY 240 ATTAATGAATCGGCCAACCGCGGGAGAGCGGCTTTCGCTATTGGCGCCAGGGTGGTT 299
Db 251 attaatgaatcgccaaacgcgcgggagagcggtttgcgtatttgggcccaggggtgtt 310
QY 300 TTTCTTTTCCAGCTGAGACGGCAACAGCTGATTGCCCTTCCAGCTGGCCCTGAGAGAG 359
Db 311 ttctttccagtgagacgagcgagcggttgccttccagctgagcgctggccctgagag 370
QY 360 AGTTGCAAGCAAGCGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
Db 371 agttgcaagcaagcggtccacgctggtttgcccacacagcgagaaatccctgttgatgg 430
QY 420 GTTCCGGAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTG 479
Db 431 gttccggaatcgcgcaaaatcccttataaatacaaaagaaatagccgagatagggttgag 490
QY 480 TTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCCAAGTCAAGAGGC 539
Db 491 ttggtccagtttggaaacaagantccactattaaagaacgtggagctccaaagggc 550
QY 540 GAAAAACGCTATCAGGCGGCTGCGCCACTTACCTGAAACCATCACCAATC 591
Db 551 gaaaaacgctctatcagggcgat -gcccaactacgtgaacatccaccacaaatc 601

RESULT 14
US-09-334-818A-5
; Sequence 5, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FY7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17

Db 9 gccaaagcttgcagctgcaggtcagactctagagatcccggtaccgagctcgaattc 68
QY 61 GTAATCATGGTCATAGCTGTTTCTCTGTGAAATTGTTATCCGCTCACAAATTCACACAA 120
Db 69 gtaatcatggtcatagctgtttctctgttgaaattgttatccgctcacattccacacaa 128
QY 121 CATACAGCGGGAAGCATAAAGTAAAGCTGGGTGCTTAATGAGTGAAGTGAAGTGAAGTGA 180
Db 129 catacagcggaagcataaagtgtaaaagcctgggtgcttaagtgaagtgagctaaactac 188
QY 181 ATTAATTCGCTTCAGTCCCGCTTTCAGTCCCGCTTTCAGTCCCGCTTTCAGTCCCGCTTTC 240
Db 189 attaatgctgtgcgtcactgccgctttccagtcgggaaacccctgtcgtgccagctgca 248
QY 241 TTAATGAATCGGCAACCGCGGAGAGCGGCTTTCGCTATTGGGCGCCAGGGTGGTTT 300
Db 249 ttaatgaatcgccaaacgcgcgggagagcggtttgctgtatggcgccaggggtggtt 308
QY 301 TTTCTTTTCCAGCTGAGACGGCAACAGCTGATTGCTTTCACCGCTGGCCCTGAGAGA 360
Db 309 ttctttccagctgagacgggcaacagctgattgccttccacgcgctggccctgagaga 368
QY 361 GTTCAGCAAGCGGTCACGCTGTTTTCGCCAGCAGCGCAAAATTCCTGTTGATGTTGG 420
Db 369 gttgcagcaagcggccacagctggtttgcccagcagcgagaaatccctgtttgatgg 428
QY 421 TTTCCGAAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 480
Db 429 ttccgaaatcggcaaaatcccttataaatacaaaagaaatagcccgagatagggttgag 488
QY 481 TGTTCAGTTTGGCAAGAGTCCACTATTAAAGAACGTGGAGTCCAGCTCAACGTCAAAGGGG 540
Db 489 tgttcagtttggaaacaga -tccactataaagaacgtggactccaaacgtcaaaagggcg 547
QY 541 AAAAAACGCTATCAGGCGGATGGCCACTACGTGACCATCACCCAA 588
Db 548 aaaaacgctctatcagggcgagggccactacgtgaancatcaccacaa 595

RESULT 13
US-09-334-818A-18
; Sequence 18, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FY7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)
; OTHER INFORMATION: a, t, c or g
; FEATURE:

Search completed: August 1, 2002, 11:04:49
Job time: 8684 sec

us-10-014-743-1.rnpn

Thu Aug 1 12:08:41 2002

Thu Aug 1 12:08:45 2002

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 10:59:18 ; Search time 4897.61 Seconds
(without alignments)
79.514 Million cell updates/sec

Title: US-10-014-743-2
Perfect score: 18
Sequence: 1 TGTAAACGCGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 74: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	1	PCT-US00-07945-5	Sequence 5, Appl
2	18	100.0	18	1	PCT-US00-33547-465	Sequence 465, App
3	18	100.0	18	1	PCT-US00-34970-12	Sequence 12, Appl
4	18	100.0	18	1	PCT-US01-04064-39	Sequence 39, Appl
5	18	100.0	18	1	PCT-US01-06056-9	Sequence 9, Appl
6	18	100.0	18	1	PCT-US01-06516-10	Sequence 10, Appl
7	18	100.0	18	1	PCT-US01-08961-84	Sequence 84, Appl
8	18	100.0	18	1	PCT-US01-09718-134	Sequence 134, App
9	18	100.0	18	1	PCT-US01-10298-49	Sequence 49, Appl
10	18	100.0	18	1	PCT-US01-10666-124	Sequence 124, App
11	18	100.0	18	1	PCT-US01-10670-54	Sequence 54, Appl
12	18	100.0	18	1	PCT-US01-10671-49	Sequence 49, Appl
13	18	100.0	18	1	PCT-US01-10742-174	Sequence 174, App
14	18	100.0	18	1	PCT-US01-11509-130	Sequence 130, App
15	18	100.0	18	1	PCT-US01-11853-79	Sequence 79, Appl
16	18	100.0	18	1	PCT-US01-11943-34	Sequence 34, Appl
17	18	100.0	18	1	PCT-US01-12011-49	Sequence 49, Appl
18	18	100.0	18	1	PCT-US01-12254A-49	Sequence 49, Appl
19	18	100.0	18	1	PCT-US01-12257-79	Sequence 79, Appl
20	18	100.0	18	1	PCT-US01-12268-29	Sequence 29, Appl
21	18	100.0	18	1	PCT-US01-12302-39	Sequence 39, Appl
22	18	100.0	18	1	PCT-US01-12303-74	Sequence 74, Appl
23	18	100.0	18	1	PCT-US01-12305-49	Sequence 49, Appl
24	18	100.0	18	1	PCT-US01-12453-69	Sequence 69, Appl
25	18	100.0	18	1	PCT-US01-14715-64	Sequence 64, Appl
26	18	100.0	18	1	PCT-US01-14772-39	Sequence 39, Appl
27	18	100.0	18	1	PCT-US01-14773-19	Sequence 19, Appl
28	18	100.0	18	1	PCT-US01-14773-19	Sequence 25, Appl
29	18	100.0	18	1	PCT-US01-15789-25	Sequence 25, Appl
30	18	100.0	18	1	PCT-US01-16045-71	Sequence 71, Appl
31	18	100.0	18	1	PCT-US01-16278-24	Sequence 24, Appl
32	18	100.0	18	1	PCT-US01-16280-99	Sequence 99, Appl

32 18 100.0 18 1 PCT-US01-16350A-34
33 18 100.0 18 1 PCT-US01-16352-89
34 18 100.0 18 1 PCT-US01-16905-34
35 18 100.0 18 1 PCT-US01-17252-124
36 18 100.0 18 1 PCT-US01-17994-79
37 18 100.0 18 1 PCT-US01-18811A-54
38 18 100.0 18 1 PCT-US01-18813-54
39 18 100.0 18 1 PCT-US01-18814-60
40 18 100.0 18 1 PCT-US01-19447A-37
41 18 100.0 18 1 PCT-US01-19835-89
42 18 100.0 18 1 PCT-US01-20951-59
43 18 100.0 18 1 PCT-US01-20952-79
44 18 100.0 18 1 PCT-US01-21064-64
45 18 100.0 18 1 PCT-US01-21306-139

ALIGNMENTS

RESULT 1
PCT-US00-07945-5
; Sequence 5, Application PC/TUS0007945
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for
; TITLE OF INVENTION: Detecting Disease of the Prostate
; FILE REFERENCE: 6397.PC.01
; CURRENT APPLICATION NUMBER: PCT/US00/07945
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/276,600
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal primer
PCT-US00-07945-5

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
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RESULT 2
PCT-US00-33547-465
; Sequence 465, Application PC/TUS0033547
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Porthury, Stuart D.
; APPLICANT: Purnan, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-228
; CURRENT APPLICATION NUMBER: PCT/US00/33547

; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
PCT-US00-33547-465

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
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RESULT 3
PCT-US00-34970-12
; Sequence 12, Application PC/TUS0034970
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0007
; CURRENT APPLICATION NUMBER: PCT/US00/34970
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,745
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
PCT-US00-34970-12

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
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RESULT 4
PCT-US01-04064-39
; Sequence 39, Application PC/TUS0104064
; GENERAL INFORMATION:
; APPLICANT: Peter J. Oefner
; TITLE OF INVENTION: DETECTION OF POLYMORPHISMS BY DENATURING
; FILE REFERENCE: STAN-174WO
; CURRENT APPLICATION NUMBER: PCT/US01/04064
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide

us-10-014-743-2.rnmpm

Thu Aug 1 12:08:45 2002

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal Primer
PCT-US01-06516-10

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

RESULT 7
PCT-US01-08961-84
; Sequence 84, Application PC/TUS0108961
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Stephen C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kishy, Beena
; APPLICANT: Klem, Stephanie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GNB3 GENE
; FILE REFERENCE: MWH-0069PCT GNB3
; CURRENT APPLICATION NUMBER: PCT/US01/08961
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/190,986
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-08961-84

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

RESULT 8
PCT-US01-09718-134
; Sequence 134, Application PC/TUS0109718
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Kishy, Beena
; APPLICANT: Klem, Stephanie E.
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Anastasio, Allison E.
; TITLE OF INVENTION: HAPLOTYPES OF THE FKBP8 GENE
; FILE REFERENCE: MWH-0072 PCT FKBP8
; CURRENT APPLICATION NUMBER: PCT/US01/09718
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,125
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134

PCT-US01-04064-39

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 5
PCT-US01-06056-9
; Sequence 9, Application PC/TUS0106056
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE DRD1 GENE
; FILE REFERENCE: MWH-0057PCT DRD1
; CURRENT APPLICATION NUMBER: PCT/US01/06056
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,922
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-06056-9

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 6
PCT-US01-06516-10
; Sequence 10, Application PC/TUS0106516
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Scroupe, Stephen D.
; TITLE OF INVENTION: Reagents And Method Useful For Detecting
; Diseases Of The Breast
; FILE REFERENCE: 5995.US.P2
; CURRENT APPLICATION NUMBER: PCT/US01/06516
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 08/962,094
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/742,667
; PRIOR FILING DATE: 1996-10-31

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-09718-134

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaaacgacgcccagt 18
|||||

RESULT 9
PCT-US01-10298-49
; Sequence 49, Application PC/TUS0110298
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Denton, R. Rex
; TITLE OF INVENTION: HAPLOTYPES OF THE GSTM3 GENE
; FILE REFERENCE: MMH-0414PCT GSTM3
; CURRENT APPLICATION NUMBER: PCT/US01/10298
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/196,830
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10298-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaaacgacgcccagt 18
|||||

RESULT 10
PCT-US01-10666-124
; Sequence 124, Application PC/TUS0110666
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kliehm, Stefanie C.
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen H.
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: HAPLOTYPES OF THE CHRN2 GENE
; FILE REFERENCE: MMH-0301PCT CHRN2
; CURRENT APPLICATION NUMBER: PCT/US01/10666
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,155
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/217,952
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10666-124

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaaacgacgcccagt 18
|||||

RESULT 11
PCT-US01-10670-54
; Sequence 54, Application PC/TUS0110670
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kliehm, Stefanie E.
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE APOA4 GENE
; FILE REFERENCE: MMH-0506PCT APOA4
; CURRENT APPLICATION NUMBER: PCT/US01/10670
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,362
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10670-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaaacgacgcccagt 18
|||||

RESULT 12
PCT-US01-10671-49
; Sequence 49, Application PC/TUS0110671
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kliehm, Stefanie E.
; APPLICANT: Koshi, Beena
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GPIA GENE
; FILE REFERENCE: MMH-0260PCT GPIA
; CURRENT APPLICATION NUMBER: PCT/US01/10671
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,341
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10671-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18

us-10-014-743-2.rnppm

Thu Aug 1 12:08:45 2002

Db 1 tgtaaacgacggccagt 18

RESULT 13
PCT-US01-10742-174
; Sequence 174, Application PC/TUS0110742
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Koshi, Beena
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Chew, Anne
; APPLICANT: Rounds, Eileen
; APPLICANT: Parks, Katie
; APPLICANT: Choi, Julie Y.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE GLCLC GENE
; FILE REFERENCE: MMH-0145 PCT GLCLC
; CURRENT APPLICATION NUMBER: PCT/US01/10742
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,305
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-10742-174

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAACGACGGCCAGT 18
Db 1 tgtaaacgacggccagt 18

RESULT 14
PCT-US01-11509-130
; Sequence 130, Application PC/TUS0111509
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Koshi, Beena
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE CALM1 GENE
; FILE REFERENCE: MMH-0102 PCT CALM1
; CURRENT APPLICATION NUMBER: PCT/US01/11509
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/196,340
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-11509-130

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAACGACGGCCAGT 18
Db 1 tgtaaacgacggccagt 18

RESULT 15
PCT-US01-11853-79
; Sequence 79, Application PC/TUS0111853
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: Haplotypes of the ACHC Gene
; FILE REFERENCE: MMH-0509 PCT ACHC
; CURRENT APPLICATION NUMBER: PCT/US01/11853
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/197,173
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-11853-79

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAACGACGGCCAGT 18
Db 1 tgtaaacgacggccagt 18

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Job time: 11351 sec

Thu Aug 1 12:08:45 2002

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us-10-014-743-2.rnpn

Thu Aug 1 12:08:45 2002

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 11:04:49 ; Search time 348.01 Seconds
(without alignments)
112.090 Million cell updates/sec

Title: US-10-014-743-2
Perfect score: 18
Sequence: 1 TGTAAACGACGGCCAGT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1353370 seqs, 1083569762 residues
Total number of hits satisfying chosen parameters: 2706740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
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7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	18	1	PCT-US02-12314-49
2	18	100.0	18	1	PCT-US02-13013-54
3	18	100.0	18	1	PCT-US02-13014-44
4	18	100.0	18	1	PCT-US02-12994-69
5	18	100.0	18	1	PCT-US02-14004-89
6	18	100.0	18	1	PCT-US02-14010-24
7	18	100.0	18	1	PCT-US02-14011-109
8	18	100.0	18	1	PCT-US02-14038-19
9	18	100.0	18	1	PCT-US02-14540-54
10	18	100.0	18	1	PCT-US02-15638-54
11	18	100.0	18	1	PCT-US02-15657-64
12	18	100.0	18	1	PCT-US01-46100A-69
13	18	100.0	18	1	PCT-US01-47011A-64
14	18	100.0	18	5	US-09-636-259A-15
15	18	100.0	18	5	US-09-120-051C-10
16	18	100.0	18	5	US-09-345-882-139
17	18	100.0	18	5	US-09-889-914A-3
18	18	100.0	18	5	US-09-431-384B-10
19	18	100.0	18	5	US-10-120-051D-10
20	18	100.0	18	6	US-10-185-567-14
21	18	100.0	18	6	US-10-192-254-13
22	18	100.0	18	6	US-10-191-045-124
23	18	100.0	18	6	US-10-069-439A-3
24	18	100.0	18	6	US-10-188-498-174
25	18	100.0	18	6	US-10-188-498-174

26	18	100.0	18	6	US-10-189-023-34	Sequence 34, Appl
27	18	100.0	18	7	US-10-022-434-16	Sequence 16, Appl
28	18	100.0	18	7	US-10-117-894-4	Sequence 4, Appl
29	18	100.0	18	7	US-10-047-412A-25	Sequence 25, Appl
30	18	100.0	18	7	US-10-126-704-139	Sequence 139, App
31	18	100.0	18	7	US-10-133-797-71	Sequence 71, Appl
32	18	100.0	18	7	US-10-151-061-6	Sequence 6, Appl
33	18	100.0	18	7	US-10-018-311A-3	Sequence 3, Appl
34	18	100.0	18	7	US-10-160-388-49	Sequence 49, Appl
35	18	100.0	18	7	US-10-160-401-29	Sequence 29, Appl
36	18	100.0	18	7	US-10-081-844-28	Sequence 28, Appl
37	18	100.0	18	7	US-10-171-888-49	Sequence 49, Appl
38	18	100.0	18	7	US-10-172-083-64	Sequence 64, Appl
39	18	100.0	18	7	US-10-176-249-124	Sequence 124, App
40	18	100.0	18	7	US-10-176-511-104	Sequence 104, App
41	18	100.0	18	7	US-10-000-467-1	Sequence 1, Appl
42	18	100.0	18	7	US-10-177-869-109	Sequence 109, App
43	18	100.0	18	7	US-10-113-956-1	Sequence 1, Appl
44	18	100.0	18	7	US-10-179-092-44	Sequence 44, Appl
45	18	100.0	18	8	US-60-384-980-589	Sequence 589, App

ALIGNMENTS

RESULT 1
PCT-US02-12314-49
; Sequence 49, Application PC/TUS0212314
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher
; APPLICANT: Lee, Helen
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE CHRM1 GENE
; FILE REFERENCE: CHRM1_MWH-0015PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/12314
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/159,269
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PCT/US00/28211
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-12314-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGGCCAGT 18
Db 1 tgtataacgacgcccagt 18
|||||

RESULT 2
PCT-US02-13013-54
; Sequence 54, Application PC/TUS0213013
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshiy, Beena
; APPLICANT: Parks, Katie
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE NRL GENE
; FILE REFERENCE: NRL_MWH-0180PCT
; CURRENT APPLICATION NUMBER: PCT/US02/13013

; CURRENT FILING DATE: 2001-04-22
; PRIOR APPLICATION NUMBER: 60/285,142
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-13013-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18
|||||

RESULT 3
PCT-US02-13014-44
; Sequence 44, Application PC/TUS0213014
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE THPO GENE
; FILE REFERENCE: THPO_MWH-0528PCT
; CURRENT APPLICATION NUMBER: PCT/US02/13014
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/285,279
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-13014-44

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18
|||||

RESULT 4
PCT-US02-12994-69
; Sequence 69, Application PC/TUS0212994
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE HCF2 GENE
; FILE REFERENCE: HCF2_MWH-0152PCT
; CURRENT APPLICATION NUMBER: PCT/US02/12994
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/285,871
; PRIOR FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-12994-69

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18
|||||

RESULT 5
PCT-US02-14004-89
; Sequence 89, Application PC/TUS0214004
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Rounds, Eileen
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRB GENE
; FILE REFERENCE: MWH-0480PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14004
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/287,960
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14004-89

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagt 18
|||||

RESULT 6
PCT-US02-14010-24
; Sequence 24, Application PC/TUS0214010
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Kliem, Stephanie E.
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE CRH GENE
; FILE REFERENCE: MWH-0249PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14010
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,476
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14010-24

Query Match 100.0%; Score 18; DB 1; Length 18;

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Thu Aug 1 12:08:45 2002

Best Local Similarity 100.0%; Pred. No. 0.33; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18

RESULT 7
PCT-US02-14011-109
; Sequence 109, Application PC/TUS0214011
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sanchis, Angela
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRA GENE
; FILE REFERENCE: MMH-0858PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14011
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,475
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14011-109

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18

RESULT 8
PCT-US02-14538-19
; Sequence 19, Application PC/TUS0214538
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE NNMT GENE
; FILE REFERENCE: MMH-0179PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14538
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 30/289,335
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14538-19

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18

RESULT 9
PCT-US02-14540-54
; Sequence 54, Application PC/TUS0214540
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Allison
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE CYP2E GENE
; FILE REFERENCE: CYP2E-MMH-0287PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14540
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,330
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14540-54

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18

RESULT 10
PCT-US02-15638-54
; Sequence 54, Application PC/TUS0215638
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Denton, R. Rex
; APPLICANT: Lee, Helen H.
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE IL8RA GENE
; FILE REFERENCE: MMH-0441PCT
; CURRENT APPLICATION NUMBER: PCT/US02/15638
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,533
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-15638-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgcccagt 18

RESULT 11
PCT-US02-15657-64
; Sequence 64, Application PC/TUS0215657
; GENERAL INFORMATION:

; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison
; APPLICANT: Rounds, Eileen
; APPLICANT: Sanchis, Angela
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE GPX2 GENE
; FILE REFERENCE: GPX2_MWH-2132PCT
; CURRENT APPLICATION NUMBER: PCT/US02/15657
; CURRENT FILING DATE: 2002-05-14
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-15657-64

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

RESULT 12
PCT-US01-46100A-69
; Sequence 69, Application PC/TUS0146100A
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Kazemi, Amir
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CER1 GENE
; FILE REFERENCE: CER1_MWH-1635PCT
; CURRENT APPLICATION NUMBER: PCT/US01/46100A
; CURRENT FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 60/241,634
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-46100A-69

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

RESULT 13
PCT-US01-47011A-64
; Sequence 64, Application PC/TUS0147011A
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Bleglecki, Karyn M
; APPLICANT: Chew, Anne
; APPLICANT: Russo, David P
; TITLE OF INVENTION: HAPLOTYPES OF THE SAH GENE
; FILE REFERENCE: SAH_MWH-1881PCT
; CURRENT APPLICATION NUMBER: PCT/US01/47011A
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,441

; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47011A-64

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 tgtaaacgacggccagt 18

RESULT 14
US-09-636-259A-15
; Sequence 15, Application US/09636259A
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2A-adrenergic receptor polymorphisms
; FILE REFERENCE: 13092
; CURRENT APPLICATION NUMBER: US/09/636,259A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-259A-15

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

RESULT 15
US-09-120-051C-10
; Sequence 10, Application US/09120051C
; GENERAL INFORMATION:
; APPLICANT: Glisson, John Robert
; APPLICANT: Luo, Yungang
; TITLE OF INVENTION: DNA encoding the outer membrane protein of Pasteurella multocida
; FILE REFERENCE: 757,003US1
; CURRENT APPLICATION NUMBER: US/09/120,051C
; CURRENT FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A primer derived from pUC18
US-09-120-051C-10

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-10-014-743-2.rnpn

Thu Aug 1 12:08:45 2002

QY 1 TGTAAACGACGGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

Search completed: August 1, 2002, 11:04:52
Job time: 8687 sec

Thu Aug 1 12:08:49 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 10:59:20 ; Search time 4897.61 Seconds
(without alignments)
3260.071 Million cell updates/sec

Title: US-10-014-743-3
Perfect score: 738
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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- 75: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	738	100.0	738	11	US-08-726-462A-3	Sequence 3, Appli
2	738	100.0	738	37	US-10-014-743-3	Sequence 6, Appli
3	723	98.0	3253	11	US-08-702-902-6	Sequence 1, Appli
4	691.8	93.7	3216	17	US-09-347-311-1	Sequence 1, Appli
5	691.8	93.7	3216	17	US-09-347-311A-1	Sequence 1, Appli
6	691.8	93.7	3216	37	US-10-057-108-1	Sequence 2, Appli
7	669.8	90.8	4885	20	US-09-539-698-2	Sequence 17, Appli
8	669	90.7	4118	14	US-09-068-821-17	Sequence 18, Appli
9	669	90.7	4118	14	US-09-068-821-18	Sequence 1, Appli
10	667.8	90.5	4539	8	PCT-US94-10146-1	Sequence 1, Appli
11	667.8	90.5	4539	15	US-09-114-835-1	Sequence 1, Appli
12	667.8	90.5	4539	15	US-09-399-593A-13	Sequence 13, Appli
13	667.8	90.5	4542	17	US-09-724-624-93	Sequence 93, Appli
14	667	90.4	2571	29	US-09-316-175-4	Sequence 4, Appli
15	666.8	90.4	8362	17	US-09-316-175-8	Sequence 8, Appli
16	666.8	90.4	8362	17	US-09-316-175-11	Sequence 11, Appli
17	666.8	90.4	10930	4	US-08-090-531-1	Sequence 12, Appli
18	666.8	90.4	10930	4	US-08-090-531-12	Sequence 11, Appli
19	666.8	90.4	10930	8	US-08-478-764-11	Sequence 12, Appli
20	666.8	90.4	10930	8	US-08-478-764-12	Sequence 9, Appli
21	666.8	90.4	10951	4	US-08-090-531-9	Sequence 10, Appli
22	666.8	90.4	10951	4	US-08-090-531-10	Sequence 9, Appli
23	666.8	90.4	10951	8	US-08-478-764-9	Sequence 10, Appli
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25	666.8	90.4	11296	17	US-09-316-175-1	Sequence 1, Appli
26	666	90.2	3323	33	US-09-860-763-8	Sequence 8, Appli
27	666	90.2	3715	33	US-09-860-763-11	Sequence 11, Appli
28	666	90.2	3774	33	US-09-860-763-9	Sequence 9, Appli
29	666	90.2	4001	33	US-09-860-763-13	Sequence 12, Appli
30	666	90.2	4107	33	US-09-861-881-1	Sequence 1, Appli
31	666	90.2	4162	33	US-09-861-881-1	Sequence 1, Appli

32 666 90.2 4393 33 US-09-861-881-2
33 666 90.2 5148 33 US-09-860-763-10
34 665.8 90.2 6688 26 US-09-667-569A-92
C 36 665.4 90.2 5115 14 US-09-020-716-5
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38 665.4 90.2 8320 26 US-09-667-569A-73
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C 41 659.4 89.3 9837 1 PCT-US97-05598-68
C 42 650.8 88.2 4161 1 PCT-US99-25666-6
C 43 650.8 88.2 4161 1 PCT-US99-25666-8
C 44 650.8 88.2 4161 15 US-09-185-143-6
C 45 650.8 88.2 4161 18 US-09-471-913-1

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Sequence 92, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 73, Appli
Sequence 72, Appli
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Sequence 68, Appli
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Sequence 8, Appli
Sequence 6, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-726-462A-3
; Sequence 3, Application US/08726462A
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Willson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08726,462A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462A-3

Query Match 100.0%; Score 738; DB 11; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.7e-205;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-10-014-743-3

; Sequence 3, Application US/10014743

; GENERAL INFORMATION:

; APPLICANT: PE Corporation (NY)

; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED FLUORESCENCE

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David J. Weitz, Willson Sonsini Goodrich

; & Rosati

; STREET: 650 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1050

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0

; SOFTWARE: Word 97

; ASCII (DOS) TEXT format

us-10-014-743-3.rnnp

Thu Aug 1 12:08:49 2002

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/014,743
 FILING DATE: 29-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/642,330
 FILING DATE: May 3, 1996
 APPLICATION NUMBER: 08/672,196
 FILING DATE: June 27, 1996
 APPLICATION NUMBER: 08/726,462
 FILING DATE: October 4, 1996
 APPLICATION NUMBER: 09/046,203
 FILING DATE: March 23, 1998
 APPLICATION NUMBER: 09/272,097
 FILING DATE: March 18, 1999
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Weltz
 REGISTRATION NUMBER: 38,362
 REFERENCE/DOCKET NUMBER: 16842-776
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 493-9300
 TELEFAX: (650) 493-6811
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 738 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-014-743-3

Query Match 100.0%; Score 738; DB 37; Length 738;
 Best Local Similarity 100.0%; Pred. No. 1.7e-205;
 Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACGACCTACATATAGGCGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60
 DB 1 ATACGACCTACATATAGGCGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60

QY 61 GCAGGATGCAAGCTTGTAGTATCTATAGTGCACCTAAATAGCTTGGCGTAATCATGTT 120
 DB 61 GCAGGATGCAAGCTTGTAGTATCTATAGTGCACCTAAATAGCTTGGCGTAATCATGTT 120

QY 121 CATAGCTGTTCTCTGTGTAATTTGTATCCGCTCACAAATCCACACATACGACCG 180
 DB 121 CATAGCTGTTCTCTGTGTAATTTGTATCCGCTCACAAATCCACACATACGACCG 180

QY 181 GAAGCATAAAGTGAAGCTGGGTGCCTAATGAGTGAAGTAACTCACTTAATTTGCT 240
 DB 181 GAAGCATAAAGTGAAGCTGGGTGCCTAATGAGTGAAGTAACTCACTTAATTTGCT 240

QY 241 TGGCTCAGTCCGCTTTCCAGTCCGGGAAACCTGCTGCGGAGCTGCATTAAATGATCG 300
 DB 241 TGGCTCAGTCCGCTTTCCAGTCCGGGAAACCTGCTGCGGAGCTGCATTAAATGATCG 300

QY 301 GCCAACCGGGGAGAGCGGTTTGGGTATGGGCTCTCTCGCTTCCTCGCTCACTG 360
 DB 301 GCCAACCGGGGAGAGCGGTTTGGGTATGGGCTCTCTCGCTTCCTCGCTCACTG 360

QY 361 ACTGCTCGCTCGCTGCTTCCGCTGCGGAGCGGATCATGCTACATCAAGCGGTAA 420
 DB 361 ACTGCTCGCTCGCTGCTTCCGCTGCGGAGCGGATCATGCTACATCAAGCGGTAA 420

QY 421 TACGGTTATCCACAGAAATCAGGGATACGAGGAAAGAAACATGTGAGCAAAAGCCAGC 480
 DB 421 TACGGTTATCCACAGAAATCAGGGATACGAGGAAAGAAACATGTGAGCAAAAGCCAGC 480

QY 481 AAAGGCCAGGAAACCGTAAAGGCGGTTGCTGCGCTTTTCCATAGGCTCCGCCCC 540
 DB 481 AAAGGCCAGGAAACCGTAAAGGCGGTTGCTGCGCTTTTCCATAGGCTCCGCCCC 540

QY 541 CTGACGAGCATCACAAAATTCAGGCTCAAGTCAGAGTGGCGAAACCGCAGGAGCTAT 600

DB 541 CTGACGAGCATCACAAAATTCAGGCTCAAGTCAGAGTGGCGAAACCGCAGGAGCTAT 600
 QY 601 AAAGATACAGGCGTTTCCCGCTGGAGAGTCCCTCGTGGCGCTCTCTGTTCCGACCTGC 660
 DB 601 AAAGATACAGGCGTTTCCCGCTGGAGAGTCCCTCGTGGCGCTCTCTGTTCCGACCTGC 660
 QY 661 CGCTTACCGGATACCTGTCCGCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCT 720
 DB 661 CGCTTACCGGATACCTGTCCGCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCT 720

QY 721 CACGCTGTAGTATCTCA 738
 DB 721 CACGCTGTAGTATCTCA 738

RESULT 3
 US-08-702-902-6
 ; Sequence 6, Application US/08702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Belfort, Marlene
 ; TITLE OF INVENTION: GENETIC SCREENS FOR INTEIN FUNCTION
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Curtis, Morris & Saiford, P.C.
 ; STREET: 530 Fifth Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM: disk
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/702,902
 ; FILING DATE: 26-AUG-1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Frommer Esq., William S.
 ; REGISTRATION NUMBER: 25,506
 ; REFERENCE/DOCKET NUMBER: 454311-2190
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)840-3333
 ; TELEFAX: (212)840-0712
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3253 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-702-902-6

Query Match 98.0%; Score 723; DB 11; Length 3253;
 Best Local Similarity 100.0%; Pred. No. 6.9e-201;
 Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GGGCGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTGCAGCTGCAGGATGCAAGCT 75
 DB 55 GGGCGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTGCAGCTGCAGGATGCAAGCT 114

QY 76 TGACTATTCTATAGTGCACCTAAATAGCTTGGCGTAATCATGTCTAGCTGTTCTCTG 135
 DB 115 TGACTATTCTATAGTGCACCTAAATAGCTTGGCGTAATCATGTCTAGCTGTTCTCTG 174

QY 136 TGTGAATTTGTATCCGCTCAATTCACACAAATACGAGCGGAGCAATAAAGTGA 195
 DB 175 TGTGAATTTGTATCCGCTCAATTCACACAAATACGAGCGGAGCAATAAAGTGA 234

QY 196 AAGCCTGGGTCCTTAATGAGTACGTAACCTACATTAATTCGCTGCTACCTGCGCC 255
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 235 AAGCCTGGGTCCTTAATGAGTACGTAACCTACATTAATTCGCTGCTACCTGCGCC 294
QY 256 CTTTCAGTCCGGAAACCTGCGTCCGAGTGCATTAATGAATCGGCAACGCGCGGGA 315
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 295 CTTTCAGTCCGGAAACCTGCGTCCGAGTGCATTAATGAATCGGCAACGCGCGGGA 354
QY 316 GAGCGGTTTGGCTATTTGGGCGCTTCTTCCGCTTCTTCCGCTACCTGCTGCGTCCG 375
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 355 GAGCGGTTTGGCTATTTGGGCGCTTCTTCCGCTTCTTCCGCTACCTGCTGCGTCCG 414
QY 376 TCGTTCGCTGCGCGAGCGGTATCAGCTTCTTCCGCTTCTTCCGCTACCTGCTGCGTCCG 435
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 415 TCGTTCGCTGCGCGAGCGGTATCAGCTTCTTCCGCTTCTTCCGCTACCTGCTGCGTCCG 474
QY 436 AATCAGGGGATACGCGAGGAAAGATGTGAGCAAAAGGCGGTAATACGTTATCCACAG 495
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 475 AATCAGGGGATACGCGAGGAAAGATGTGAGCAAAAGGCGGTAATACGTTATCCACAG 534
QY 496 GTAAAAGGCGGTTGCTGGCGTTTTCATAGGCTCCGCGCTTCCGCGTACGAGCATCACA 555
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 535 GTAAAAGGCGGTTGCTGGCGTTTTCATAGGCTCCGCGCTTCCGCGTACGAGCATCACA 594
QY 556 AATATCGAGCTCAAGTACAGAGTGGGAAACCCGACAGGACTATAAGATACACAGCGT 615
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 595 AATATCGAGCTCAAGTACAGAGTGGGAAACCCGACAGGACTATAAGATACACAGCGT 654
QY 616 TTCCCGCTGGAAGCTCCCTGCTGGCTCTCTCTGTCGAGCCTGCGGTTACCGGATACC 675
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 655 TTCCCGCTGGAAGCTCCCTGCTGGCTCTCTCTGTCGAGCCTGCGGTTACCGGATACC 714
QY 676 TGTCGCGCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCTATAGGCTCCGCGTACGAGCATCACA 735
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 715 TGTCGCGCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCTATAGGCTCCGCGTACGAGCATCACA 774
QY 736 TCA 738
Db ||||
QY 775 TCA 777

RESULT 4

US-09-347-311-1
; Sequence 1, Application US/09347311
; GENERAL INFORMATION:
; APPLICANT: Plaetnick, Geert
; APPLICANT: Plattewu, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: Characterisation of Gene Function using dsRNA
; FILE REFERENCE: 50897/002/
; CURRENT APPLICATION NUMBER: US/09/347,311
; EARLIER FILING DATE: 1999-07-02
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid DNA
US-09-347-311-1

Query Match 93.7%; Score 691.8; DB 17; Length 3216;
Best Local Similarity 96.2%; Pred. No. 9.8e-192;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;

QY 1 ATACGACTACTATPAGGCGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GCAGGC-----ATGCAAGCTTGAGTATCTATAGTGTACCAATAAATAG 103
Db |||
QY 104 CTGGCGTAAATCATGCTCATAGCTGTTCTGTGTGAAATTTCTATCCCTCACAATTC 163
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 164 ACACAACATPACGAGCGGAGCATAAAGTGTAAAGCTGGGCTCTAATGAGTACGCTA 223
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 224 ACTCATTAATTTGGCTTTCGCTCTACTCCGCTGTTTCCAGTCGGGAAACCTGTCTG 283
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 283 actcacataatgcttgcgtcactcactcactcactcactcactcactcactcactcactc 985
QY 284 GCTGCTTAATTAATTCGCGCAACGCGGCGGAGAGGCGGTTTGCCTATTTGGCGCTCT 343
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 344 GCTGCTTCTGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1045
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1046 cgtctctcactcactcactcactcactcactcactcactcactcactcactcactc 403
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 404 TCACCTAAAGCGGCTTAATACGTTATCCACAGATCAGGCGGTAACACGAGAAAGAACAT 463
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 464 GTGAGCAAAAGGCGGCAAGAACGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 524 CCATAGGCTCCGCGCGCTGAGGAGCATCAGGAGTAAAGGCGGCTGCTGCTGCTGCTGCT 1225
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1226 cgtatggtcgc 583
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 584 AAACCGCAGAGCTATTAAGATACGAGCGGTTTCCCGCTGGAAGCTCCCTGCTGCTGCT 1285
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1286 aaacccgacagactataaagataccagcgcttcccccctggaagcctccctcgcgcgc 643
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 644 TCGTGTCCGAGCCCTGCGCTTACCGGATACCTGTCGCCCTTTTCCTTCCTTCGGAAGCGT 1345
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1346 tctgttcgc 703
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 704 GCGCTTTCATAGCTACCTGTAGGTATCTCA 738
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1406 ggcgcttctcatagctcagctgtaggtatctca 1440

RESULT 5

US-09-347-311A-1
; Sequence 1, Application US/09347311A
; GENERAL INFORMATION:
; APPLICANT: Plaetnick, Geert
; APPLICANT: Plattewu, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: Characterisation of Gene Function using dsRNA
; FILE REFERENCE: D0590/7003
; CURRENT APPLICATION NUMBER: US/09/347,311A
; EARLIER FILING DATE: 1999-07-02
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

;; LENGTH: 3216
;; TYPE: DNA
;; ORGANISM: Art
;; FEATURE:
;; OTHER INFORMATION:
US-09-347-311A-1

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Query Match          93.7%; Score 691.8; DB 17; Length 3216;
Best Local Similarity 96.2%; Pred. No. 9.8e-192;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;
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RESULT 6

US-10-057-108-1
; Sequence 1, Application US/10057108
; GENERAL INFORMATION:
; APPLICANT: Plaelinck, Geert
; APPLICANT: Platteeuw, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry

QY 704 GCGCTTCTCATAGCTCAGCTGATGATCTCA 738
Db 1406 ggcgtttctcatagctcaagctgagtatctca 1440

RESULT

US-09-539-698-2
; Sequence 2, Application US/09539698
; GENERAL INFORMATION:
; APPLICANT: GenStar Therapeutics Corporation
; APPLICANT: Alemany, Ramon
; APPLICANT: Fang, Xiangming
; APPLICANT: Zhang, Wei-wei
; APPLICANT: Robert, Sobol
; TITLE OF INVENTION: Complementary-Adenoviral Vector System
; FILE REFERENCE: 97-087-B
; CURRENT APPLICATION NUMBER: US/09/539,698
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/797,160
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4885
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4885)
; OTHER INFORMATION: plasmid pGT8015
; NAME/KEY: misc_feature
; LOCATION: (148)..(933)
; OTHER INFORMATION: coding sequence (CDS) for human B7-1
; NAME/KEY: misc_feature
; LOCATION: (70)..(147)
; OTHER INFORMATION: coding sequence (CDS) for transmembrane protein B1 signal peptide
; NAME/KEY: rep_origin
; LOCATION: (1466)..(2049)
; OTHER INFORMATION: complement (1466..2049) / ColE1 origin
; NAME/KEY: misc_feature
; LOCATION: (3117)..(4244)
; OTHER INFORMATION: coding sequence (CDS) for Kanamycin resistance in 4244..3117 orle
; OTHER INFORMATION: n
; NAME/KEY: misc_feature
; LOCATION: (2239)..(3099)
; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 orientati
; OTHER INFORMATION: o
; NAME/KEY: rep_origin
; LOCATION: (4245)..(4659)
; OTHER INFORMATION: complement (4245-4659) / F1 origin
US-09-539-698-2

Query Match 90.8%; Score 669.8; DB 20; Length 4885;
Best Local Similarity 95.68; Pred. No. 3.2e-185;
Matches 689; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 18 GCGAATTCAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCGATGCAAGCTTG 77
Db 961 gcacacggcggtactagtggatccgagctcggtaccagcttgatgcatgcttg 1020
QY 78 AGTATTCTATAGTGTCACTAAATAGCTTGGCGTAATCATGTGTATAGCTGTTCCTGTG 137
Db 1021 agtattctatagtgtaacctaaatagcttggcgtaactggtatgctgttctcgtg 1080
QY 138 TGAATTTGTTATCGGCTCACAAATTCACACATAGCAGCGGGAAGCATAAAGTGTA 197
Db 1081 tgaattgttatccgctcacaaatccacacacatagcagcggaagcataaagtgtaaa 1140
QY 198 GCCTGGGGTGCCTAAATCAGTGTACTACATTAATTCGCTGCGCTACTGCCCGCT 257
Db 1141 gcttgggtgcctaaatgagtgagctaaactcacattaatgctgtgctcactgcccgt 1200

QY 258 TTCCAGTCGGGAAACCTGTGTCGACGTGCATTAAATCGCCGCAACGCGCGGAGAGA 317
Db 1201 ttccagtcgggaaacctgtgtccagctgcattaaagaaacgccaacgcggggaga 1260
QY 318 GCGGCTTTGCGTATTTGGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTGCGTCGTC 377
Db 1261 ggcgggttgcgtattggcgctcttccgcttccctcgtcactgactcgtcgtcgtc 1320
QY 378 GTTCGGCTGCGGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGAA 437
Db 1321 gttcggctcggcgagcggtatcagctcactcaaaagcggtatacagtttatccacaga 1380
QY 438 TCAGGGGATAACGACGAGGAAGAACATGTGAGCAAAAGGCGCAGCAAGCAACCGT 497
Db 1381 tcaggggataacgaggaagaacatgtgagcaaaagcgcaaaagcccaaggaaccgt 1440
QY 498 AAAAAAGCGCGCTTGTGCGGCTTTTCCATAGCTCCGCCCTCCCTGACGAGCATCAAAA 557
Db 1441 aaaaagcgcgctgtgctggcggttttccatagctccgccccctgacgagcatcaaa 1500
QY 558 AATCAGCTCAAGTCAGAGGTGGGAAACCGCAGAGGACTATAAAGATACCAAGCGCTT 617
Db 1501 aatcagctcaagtgcaggggtggcgaaacccgacaggaactataagataccagggcgtt 1560
QY 618 CCCCTGGAAGCTCCCTCGCTGCTCTCTGTTCCGACCTGCCCTTACCGGATACCTG 677
Db 1561 cccctggaaagctccctcgtcgtcctcgttccgacctgtccgacctgacctgacctg 1620
QY 678 TCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGATAGTATCTC 737
Db 1621 tccgctttctcccttcgggaagcgtggcgcttctcctatagctcagctgtaggtatctc 1680
QY 738 A 738
Db 1681 a 1681

RESULT

US-09-068-821-17
; Sequence 17, Application US/09068821
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method of quantifying tumour
; TITLE OF INVENTION: cells in a body fluid and a suitable test kit
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PADAT Sequenzmodul Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,821
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 42 795.5
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 7249-1501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

Db 1482 GTGGCAACCGACAGCACTATTAAGATACAGCGGTTTCCCGCTTCCCGCTGGAAGCTCCCTCGT 1541
QY 638 CGGCTCTCTCTTCCGACCCCTGCGCTTACGGATACCTGTCCGCTTTCCTTCCTTCGGG 697
Db 1542 CGGCTCTCTCTTCCGACCCCTGCGCTTACGGATACCTGTCCGCTTTCCTTCCTTCGGG 1601
QY 698 AAGGTGCGGCTTCTCATAGCTCAGCGTGTAGGTATCTCA 738
Db 1602 AAGGTGCGGCTTCTCATAGCTCAGCGTGTAGGTATCTCA 1642

RESULT 10
PCT-US94-10146-1
: Sequence 1, Application PC/TUS9410146
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Intron Mediated Recombinant Techniques and
: TITLE OF INVENTION: Reagents
: NUMBER OF SEQUENCES: 3
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10146
: FILING DATE: 12-SEPT-1994
: CLASSIFICATION:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4539 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: other nucleic acid
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 969..1259
: OTHER INFORMATION: /product= "E3 exon"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1290..1559
: OTHER INFORMATION: /product= "E5 exon"
PCT-US94-10146-1

Query Match 90.5%; Score 667.8; DB 1; Length 4539;
Best Local Similarity 97.9%; Pred. No. 1.2e-184;
Matches 688; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 39 GGGATCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGAGTATCTATAGTGTACACCTA 98
Db 2235 GGGATCTCTAGAGTCGACCTGCAGGCATGCAAGCTTTTGTTCCTTTAGTGAGGGTTA 2294
QY 99 AAT---AGCTTGGGTAATCATGTGTCATAGCTTTCCTGTGTGAAATTTATCCGCTC 155
Db 2295 ATTTCGAGCTTGGGTAATCATGTGTCATAGCTTTCCTGTGTGAAATTTATCCGCTC 2354
QY 156 ACAATTCACACATACACGAGCGGAGCATAAAGTGTAAAGCTGGGTCCTTAATGA 215
Db 2355 ACAATTCACACATACACGAGCGGAGCATAAAGTGTAAAGCTGGGTCCTTAATGA 2414
QY 216 GTGAGCTAACTACATTAATTTGGCTTGGCTTTCCTGCTTTCCTGCTGCGGAAACCTG 275
Db 2415 GTGAGCTAACTACATTAATTTGGCTTGGCTTTCCTGCTTTCCTGCTGCGGAAACCTG 2474
QY 276 TCGTGCAGCTGCAATTAATGAATCGGCAACGCGCGGAGAGCGGTTTCGGTATTGGG 335
Db 2475 TCGTGCAGCTGCAATTAATGAATCGGCAACGCGCGGAGAGCGGTTTCGGTATTGGG 2534
QY 336 CGCTCTTCCGCTTCCCTGCTCACTGACTCGCTGCGCTCGGTCGCTGCGCTGCGCGAGCG 395
Db 2535 CGCTCTTCCGCTTCCCTGCTCACTGACTCGCTGCGCTCGGTCGCTGCGCTGCGCGAGCG 2594

QY 396 GTATCAGCTCACTCAAGGCGGTAAATACGGTTATTCACAGAAATACAGGGGATAACGAGGA 455
Db 2595 GTATCAGCTCACTCAAGGCGGTAAATACGGTTATTCACAGAAATACAGGGGATAACGAGGA 2654
QY 456 AAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGGTTAAAGGCGGTTGCTG 515
Db 2655 AAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGCAAAAGGCGGTTAAAGGCGGTTGCTG 2714
QY 516 GCGTTTTTCCATAGGCTCGCCCTCGAGCATCAACAAATCGAGCTCAAGCTCAG 575
Db 2715 GCGTTTTTCCATAGGCTCGCCCTCGAGCATCAACAAATCGAGCTCAAGCTCAG 2774
QY 576 AGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTC 635
Db 2775 AGGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTC 2834
QY 636 GTGGCTCTCTCTGTTCGACCTGCGCTTACCGGATACCTGCGCTTCTCCCTTCGCTTCG 595
Db 2835 GTGGCTCTCTCTGTTCGACCTGCGCTTACCGGATACCTGCGCTTCTCCCTTCGCTTCG 2894
QY 596 GGAAGCTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 738
Db 2895 GGAAGCTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 2937

RESULT 11
US-08-488-015-1
: Sequence 1, Application US/08488015
: GENERAL INFORMATION:
: APPLICANT: Jarrell, Kevin A.
: TITLE OF INVENTION: INTRON MEDIATED RECOMBINANT TECHNIQUES
: TITLE OF INVENTION: AND REAGENTS
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,015
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: HUI-008CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4539 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: other nucleic acid
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 969..1259
: OTHER INFORMATION: /product= "E3 exon"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1290..1559
: OTHER INFORMATION: /product= "E5 exon"
US-08-488-015-1

QY 636 GTGGCTCTCTGTTCCGACCTGCGCTTACCGATACCTGTCGGCTCTTCTCCCTTCG 695
Db 2835 GTGGCTCTCTGTTCCGACCTGCGCTTACCGATACCTGTCGGCTCTTCTCCCTTCG 2894
QY 696 GGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 738
Db 2895 GGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 2937

RESULT 13

US-09-399-593A-13
; Sequence 13, Application US/09399593A
; GENERAL INFORMATION:
; APPLICANT: Jarrell Ph.D., Kevin A
; APPLICANT: Mikheeva, Svetlana
; APPLICANT: Donahue, William
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES AND REAGENTS
; FILE REFERENCE: Ribozyme shuffling; improvments, in vivo
; CURRENT APPLICATION NUMBER: US/09/399,593A
; CURRENT FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4542
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pIN1 plasmid
US-09-399-593A-13

Query Match 90.5%; Score 667.8; DB 17; Length 4542;
Best Local Similarity 97.9%; Pred. No. 1.2e-184;
Matches 688; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 39 GGGGATCCTCTAGAGTCGACCTGCGAGGATGCAAGCTTGAGTATCTATAGTGCACCTA 98
Db 2238 ggggattcctctagagtcgacctgagcgatgcaagctttgttcccttagtgagggtta 2297
QY 99 AAT---AGCTTGGCGTAAATCATAGTGTATAGTGTGCTGCTGCAAAATTTGATCCGCTC 155
Db 2298 attcgagcttgcgtaatacatggtcatagctgttccctgtgtaaatgttcatccgctc 2357
QY 156 ACAATCCACACATACAGCGCGGAGGATGAAGTGTAAAGCTTGGGTGCGCTAATGA 215
Db 2358 acaattccacacatacagcgcgagcgcgataaagtgtaaagcctggggtgcctaata 2417
QY 216 GTGAGCTAACTACATTAATTTGGTGTGCGCTCACTGCGCGCTTCCAGTCCGGAAACCTG 275
Db 2418 gtgagtaactcacatttaatttggtgtgctcaactgcccgtcttcagtcgggaaacctg 2477
QY 276 TCGTGCAGCTGCATTAATTCGCCCAACGCGCGGAGAGCGGTTTGCCTATTGGG 335
Db 2478 tcgtgccagctgcatttaataatcgcccaacgcgcgggagagcggtttggtatg99 2537
QY 336 CGCTCTTCGCTTCCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
Db 2538 cgccttcgcgttcctcgcctcaactgactgctgctgctgctgctgctgctgctgctgctg 2597
QY 396 GTATCAGCTCACTCAAGCGCGTAAATACGGTTATCCAGAAATCAGGGGATACGCGAGGA 455
Db 2598 gtatcagctcaactcaagcggttaatacggttatccagaaatcagagataacgagga 2657
QY 456 AAGAACTGTGAGCAAAAGGCGCAGCAAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 515
Db 2658 aagaaca tgtgagcaaaagccagcaaaagccagcaaaagccagcaaaagccagcaaaag 2717
QY 516 GCGTTTTCATAGCTCCGCCCTCGACGAGCATCAAAAATTCAGCGCTCAAGTTCAG 575
Db 2718 gcgttttccatagctccgccctcgacgagcatcaaaaaatcagcgtcaagtcag 2777
QY 576 AGGTGCGAAACCCGACGAGGACTATAAAGATACCGAGCGTTTCCCTCGGAGCTCCCTC 635

Db 2778 aggttgccgaaacccacaggaactataaagataccagcgcttcccccctggaagctccctc 2837
QY 636 GTGGCTCTCTGTTCCGACCTGCGCTTACCGATACCTGTCGGCTCTTCTCCCTTCG 695
Db 2835 GTGGCTCTCTGTTCCGACCTGCGCTTACCGATACCTGTCGGCTCTTCTCCCTTCG 2894
QY 696 GGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 738
Db 2895 GGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 2937

RESULT 14

US-09-724-624-93/c
; Sequence 93, Application US/09724624
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: Modification of Gene Expression
; CURRENT APPLICATION NUMBER: US/09/724,624
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-724-624-93

Query Match 90.4%; Score 667; DB 29; Length 2571;
Best Local Similarity 100.0%; Pred. No. 1.7e-184;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 AGCTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAAATCATAGTGCATAGCTGTTT 131
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QY 132 CCTGTGTGAATTTATTCGCTCACAAATTCACACAAATACGAGCGGAGGATAAAG 191
Db 872 CCTGTGTGAATTTATTCGCTCACAAATTCACACAAATACGAGCGGAGGATAAAG 813
QY 192 TGTAAAGCCTGGGTGCTTAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 251
Db 812 TGTAAAGCCTGGGTGCTTAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 753
QY 252 CCGCTTTTCCAGTGGGAAACCTGTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 752 CCGCTTTTCCAGTGGGAAACCTGTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
QY 312 GGGAGAGGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTG 371
Db 692 GGGAGAGGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTG 633
QY 372 TCGGTGTTTCGCTGCGGAGCGGTATCAGCTCAAGCGGTATCAGCTCAAGCGGTATCAGCT 431
Db 632 TCGGTGTTTCGCTGCGGAGCGGTATCAGCTCAAGCGGTATCAGCTCAAGCGGTATCAGCT 573
QY 432 ACAGAAATCAGGGAATACCGCAGGAAAGACATGTGAGCAAAAGGCGGAGGCGGAGGCGG 491
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5601	Db	agaaacatgtgagcaaaaaggccagcaaaagccgaagacgttaaaaagggccggttgcgcgg	5660
517	QY	CGTTTTTCATAGGCTCCGCCCCCTGACGAGGATCATCAAAAATCGACGCTCAAGTCAAG	576
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577	QY	GGTGGCGAAACCGACAGGACTATAAAGATACCAAGCGGTTTCCCCCTGGGAAGCTCCCTCG	636
5721	Db	gg tggcgaaacccgacaggactataagataccaggcggtttccccttggagctccctcg	5780
637	QY	TGCGCTCTCCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGG	696
5781	Db	tgcgcctcctgtttccgaacctgcccgttacgggatacctgcccgcctttctcccttcgg	5840
697	QY	GAACGCTGGCGCTTCTCATAGCTACGCTGAGGTATCTCA	738
5841	Db	gaagcgttgggcgtttctcatagctcaacgtgtagtatctca	5882

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RESULT 15
US-09-316-175-4
; Sequence 4, Application US/09316175
; GENERAL INFORMATION:
; APPLICANT: Osorio, Jorge E.
; APPLICANT: Dryga, Sergey
; TITLE OF INVENTION: RECOMBINANT MENO VIRUS GENOMES, MENO VIRUS REPLICONS,
; TITLE OF INVENTION: PACKAGED REPLICON PARTICLES, AND NUCLEIC ACID-BASED
; TITLE OF INVENTION: DELIVERY VEHICLES
; FILE REFERENCE: DE-2-C1
; CURRENT APPLICATION NUMBER: US/09/316.175
; CURRENT FILING DATE: 1999-05-21
; EARLIER APPLICATION NUMBER: 60/086.271
; EARLIER FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8362
; TYPE: DNA
; ORGANISM: Mengo virus
US-09-316-175-4

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Query Match	90.4%	Score	666.8	DB	17	Length	8362
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QY	277	CGTGCACAGTGCATTAAATCGGCCAACCGCGGGGAGAGCGCGTTCGCTATTGGGC	336				
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QY	337	GCTCTCCGCTTCTCTCGCTCACGTACTCGCTGCTCGCTCGCTCGTTCGCTCGCTCGCGAGCGG	396				
DB	5481	gctctccgcgttccctcgctcactgcactgcgtgcgcctcggtcggttcggtcggcgcgagcgg	5540				

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
4595.698 Million cell updates/sec

Title: US-10-014-743-3

Perfect score: 738

Sequence: 1 ATACGACTACATATAGGCGG.....CTCAGCGTGTAGGTATCTCA 738

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1353370 seqs, 1083569762 residues

Total number of hits satisfying chosen parameters: 2706740

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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 - 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
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 - 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
 - 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	669.8	90.8	4885	US-09-539-698A-2	Sequence 2, Appli
2	667	90.4	2571	US-10-137-036-93	Sequence 93, Appl
3	667	90.4	3018	US-09-486-142-7	Sequence 7, Appli
4	667	90.4	3357	PCT-US02-17452-96	Sequence 96, Appl
5	667	90.4	3357	PCT-US02-17451-7	Sequence 7, Appli
6	667	90.4	3357	US-10-161-403-96	Sequence 96, Appl
7	667	90.4	3357	US-10-161-408-7	Sequence 7, Appli
8	666.8	90.4	8017	US-10-152-040-26	Sequence 26, Appl
9	666.8	90.4	8092	US-10-152-040-27	Sequence 27, Appl
10	665.8	90.4	10417	US-10-152-040-28	Sequence 28, Appl
11	665.8	90.2	6688	US-09-813-453A-72	Sequence 72, Appl
12	665.4	90.2	4606	PCT-US02-21336-27	Sequence 27, Appl
13	665.4	90.2	5983	PCT-US02-21336-30	Sequence 30, Appl
14	665.4	90.2	8320	US-09-813-453A-71	Sequence 71, Appl
15	645.8	87.5	2713	PCT-US02-17452-32	Sequence 32, Appl
16	645.8	87.5	2713	PCT-US02-17451-23	Sequence 23, Appl
17	645.8	87.5	2713	US-10-161-403-32	Sequence 32, Appl
18	645.8	87.5	2713	US-10-161-408-23	Sequence 23, Appl
19	638.2	86.5	7175	US-10-110-504-13	Sequence 13, Appl
20	638	86.4	3858	US-10-110-504-33	Sequence 33, Appl
21	638	86.4	4960	US-09-756-577-29	Sequence 29, Appl
22	638	86.4	5711	US-10-110-504-21	Sequence 21, Appl
23	638	86.4	7332	US-09-756-577-30	Sequence 30, Appl
24	637.6	86.4	8108	US-10-121-988-77	Sequence 77, Appl
25	637	86.3	3599	US-09-861-101B-3	Sequence 3, Appli

26	637	86.3	3600	5	US-09-861-101B-2	Sequence 2, Appli
27	637	86.3	3796	7	US-10-127-391-32	Sequence 32, Appl
28	637	86.3	4346	1	PCT-US02-17452-113	Sequence 113, Appl
29	637	86.3	4346	1	PCT-US02-17451-26	Sequence 26, Appl
30	637	86.3	4346	7	US-10-161-403-113	Sequence 113, Appl
31	637	86.3	4346	7	US-10-161-408-26	Sequence 26, Appl
32	637	86.3	4704	5	US-09-932-328-4	Sequence 4, Appli
33	637	86.3	5382	5	US-09-479-123-21	Sequence 21, Appl
34	637	86.3	5382	5	US-09-513-574-21	Sequence 21, Appl
35	637	86.3	5618	5	US-09-570-546-1	Sequence 1, Appli
36	637	86.3	6367	7	US-10-142-358-1	Sequence 1, Appli
37	637	86.3	6367	7	US-10-050-227-1	Sequence 2, Appli
38	637	86.3	6926	7	US-10-050-227-2	Sequence 6, Appli
39	637	86.3	7228	1	PCT-US02-15239-6	Sequence 16, Appl
40	637	86.3	7573	7	US-10-110-504-16	Sequence 30, Appl
41	637	86.3	7573	7	US-10-110-504-30	Sequence 32, Appl
42	637	86.3	8062	7	US-10-110-504-32	Sequence 31, Appl
43	637	86.3	8153	7	US-10-110-504-31	Sequence 8, Appli
44	637	86.3	8937	1	PCT-US02-17258-8	Sequence 9, Appli
45	637	86.3	8937	1	PCT-US02-17258-9	

ALIGNMENTS

RESULT 1
US-09-539-698A-2
; Sequence 2, Application US/09539698A
; GENERAL INFORMATION:
; APPLICANT: Genstar Therapeutics Corporation
; APPLICANT: Alemany, Ramon
; APPLICANT: Fang, Xiangming
; APPLICANT: Zhang, Wei-Wei
; APPLICANT: Robert, Sobol
; TITLE OF INVENTION: Complementary-Adenoviral Vector System
; FILE REFERENCE: 97-087-B
; CURRENT APPLICATION NUMBER: US/09/539,698A
; PRIOR FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4885
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4885)
; OTHER INFORMATION: plasmid pCT8015
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (148)..(933)
; OTHER INFORMATION: coding sequence (CDS) for human B7-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(147)
; OTHER INFORMATION: coding sequence (CDS) for transmembrane protein B1 signal pe
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1466)..(2049)
; OTHER INFORMATION: complement (1466..2049) / ColE1 origin
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3117)..(4244)
; OTHER INFORMATION: coding sequence (CDS) for kanamycin resistance in 4244..311
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2239)..(3099)
; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 ori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2239)..(3099)
; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 ori
; FEATURE:

; NAME/KEY: rep_origin
; LOCATION: (4245)...(4659)
; OTHER INFORMATION: complement (4245-4659) / F1 origin
US-09-539-698A-2

Query Match 90.8%; Score 669.8; DB 5; Length 4885;
Best Local Similarity 95.6%; Pred. No. 3.5e-185;
Matches 689; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 18 GCGAATTCGAGCTCGGTCCCGGGATCCTCTAGAGTGACCTGAGGCGATCGAAGCTTG 77
DB 961 gcacactggcgccgttactagtcgagctgcgagctgcacagcttgatgcatagcttg 1020
QY 78 AGTATTCATAGTGACCTAAATAGCTGGGTAATATGTCATGTCATGCTGTTTCTCTG 137
DB 1021 agtatctatagtgcaactaaatagctggcgtaatactgctatgctgtctctctg 1080
QY 138 TGAATTCCTATCGCTCACATTCACACATACGAGCGGGAAGCATAAAGTGTA 197
DB 1081 tgaattgtttatccgctcacattccacacacatacagccggaagcataaaagtgt 1140
QY 198 GCCTGGGTGCTAATGAGTGAGCTAAGTACATTAATTCGCTGCTGCTGCTGCTG 257
DB 1141 gctgggtgctaatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1200
QY 258 TTCAGTCCGGGAACCTGCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
DB 1201 ttccagtcgggaacacctgctgctgctgctgctgctgctgctgctgctgctgctg 1260
QY 318 GCGGTTTGGCTATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 377
DB 1261 ggcgtttgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1320
QY 378 GTTCGCTGCGGAGCGGTATGAGTCACTCAAGCGGTATATGCTGCTGCTGCTGCTG 437
DB 1321 gtcgctgctgagcggtatgagtcactcaagcggtatgagtcactcaagcggtatg 1380
QY 438 TCAGGGGATTAACGAGGAAAGACATGTGACAAAGGCGGAGGAGGAGGAGGAGGAG 497
DB 1381 tcaggggataacgaggaagaaacatgtgagcaaaagggcgagcaaaagggcgag 1440
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DB 1621 tccgcttttctcccttccgggaagcggtggcgctttctcatagctacgctgtagg 1680
QY 738 A 738
DB 1681 a 1681

RESULT 2
US-10-137-036-93/c
; Sequence 93. Application US/10137036
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth

; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-137-036-93

Query Match 90.4%; Score 667; DB 7; Length 2571;
Best Local Similarity 100.0%; Pred. No. 2e-184;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 AGCTTGAGTATTCATAGTGTACCTTAATAGCTTGGCGTAATCATAGCTGTTT 131
DB 932 AGCTTGAGTATTCATAGTGTACCTTAATAGCTTGGCGTAATCATAGCTGTTT 873
QY 132 CCTGTGAAATGTTATCCGCTCACAATTCACACACATACGAGCGGAAGCATAAG 191
DB 872 CCTGTGAAATGTTATCCGCTCACAATTCACACACATACGAGCGGAAGCATAAG 813
QY 192 TGTAAAGCTGGGCTGCTTAATGAGTGAGCTAACTCACTTAATTCGCTGCTGCTG 251
DB 812 TGTAAAGCTGGGCTGCTTAATGAGTGAGCTAACTCACTTAATTCGCTGCTGCTG 753
QY 252 CCCTGCTTCCAGTGGGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
DB 752 CCCTGCTTCCAGTGGGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693
QY 312 GGAGAGGCGGTTGCGTATTTGGCGCTCTTCCGCTTCTGCTGCTGCTGCTGCTGCTG 371
DB 692 GGAGAGGCGGTTGCGTATTTGGCGCTCTTCCGCTTCTGCTGCTGCTGCTGCTGCTG 633
QY 372 TCCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
DB 632 TCCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
QY 432 ACAGATACAGGCGATACGCGAGAAAGACATGTGAGCAAAAGGCCAGCAAGGCCAGG 491
DB 572 ACAGATACAGGCGATACGCGAGAAAGACATGTGAGCAAAAGGCCAGCAAGGCCAGG 513
QY 492 AACCGTAAAGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
DB 512 AACCGTAAAGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 453
QY 552 CACAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATATAAGATACCAG 611
DB 452 CACAAAATCGAGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATATAAGATACCAG 393
QY 612 GCGTTTCCCTTGGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 671
DB 392 GCGTTTCCCTTGGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
QY 672 TACCTGTCGCGCTTCTCCCTTCCGGAAGCGTGGGCGCTTCTCTCATAGCTCAGCTGCTAGG 731
DB 332 TACCTGTCGCGCTTCTCCCTTCCGGAAGCGTGGGCGCTTCTCTCATAGCTCAGCTGCTAGG 273

Db 669 gegtccccctggaagctccctcgtcgtctcctctcgtccgacccctgacgctgacgga 728
 QY 672 TACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTACGCTGTAGG 731
 Db 729 tacctgtccgctctctcctcctcctcgtggaagcgtggtcgtctcctcgtcgtcgtgag 788
 QY 732 TATCTCA 738
 Db 789 tatctca 795

RESULT 4

PCT-US02-17452-96
 ; Sequence 96, Application PC/TUS0217452
 ; GENERAL INFORMATION:
 ; APPLICANT: CHROMOS MOLECULAR SYSTEMS, INC.
 ; APPLICANT: Perkins, Edward
 ; APPLICANT: Perez, Carl
 ; APPLICANT: Lindenbaum, Michael
 ; APPLICANT: Greene, Amy
 ; APPLICANT: Leung, Josephine
 ; APPLICANT: Fleming, Elena
 ; APPLICANT: Stewart, Sandra
 ; APPLICANT: Shellard, Joan
 ; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
 ; FILE REFERENCE: 24601-420PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/17452
 ; CURRENT FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/294,758
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: 60/366,891
 ; PRIOR FILING DATE: 2002-03-21
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 96
 ; LENGTH: 3357
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: pGEMeasyNOS Plasmid
 PCT-US02-17452-96

Query Match 90.4%; Score 667; DB 1; Length 3357;
 Best Local Similarity 100.0%; Pred. No. 2.1e-184; Indels 0; Gaps 0;
 Matches 667; Conservative 0; Mismatches 0

QY 72 AGCTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTGTATAGTGT 131
 Db 70 agcttgagtattctatagtgctacacataatgctggttaataatgctggttt 129
 QY 132 CTTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACAGCGGGAAGCAAT 191
 Db 130 cctgtgtgaattgtttatccgctcacataatccacacatacagcggaagcataag 189
 QY 192 TGTAAAGCCTGGGTGCTTAAATGAGTGAAGTCACTAAATTTCCGCTTCCGCTCACTG 251
 Db 190 tgaagagcctgggtgcttaataatgagctcaacacataatgagtggtggtcactg 249
 QY 252 CCGCTTTTCCAGCTCGGGAACCTGCTGCGCAAGTGCATTAATGAATCGGCAACGCCGCG 311
 Db 250 cccgctttccagctcggaacacctgctgcccagctgcttaataatgagtggtggtc 309
 QY 312 GGGAGAGCGGTTTGGGCTTATTTGGGCGCTTCTCCGCTTCCGCTCACTGCTGCGCG 371
 Db 310 gggagagcggtttgctgattggcgctctccgcttccgctcactgactgactgctg 369
 QY 372 TCGGTGCTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGCTTATCC 431
 Db 370 tcgggtcgctcggtcggtgagcggtatcagctcactcaaaagcggttaataatggttacc 429
 QY 432 ACAGAAATCAGGGGATTAACGAGCAAGAAACATGTGTAGCAAAAGGCCAGCAAAAGGCCAGG 491

QY 732 TATCTCA 738
 Db 272 TATCTCA 266
 RESULT 3
 US-09-486-142-7
 ; Sequence 7, Application US/09486142
 ; GENERAL INFORMATION:
 ; APPLICANT: Martinez, Jean
 ; APPLICANT: Goze, Catherine
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR IDENTIFYING PRECURSORS OF AMIDATED POLYPEPT
 ; TITLE OF INVENTION: HORMONES
 ; FILE REFERENCE: 427, 034
 ; CURRENT APPLICATION NUMBER: US/09/486,142
 ; CURRENT FILING DATE: 2002-06-11
 ; PRIOR APPLICATION NUMBER: PCT/FR98/01767
 ; PRIOR FILING DATE: 1998-08-07
 ; PRIOR APPLICATION NUMBER: FR 97/10643
 ; PRIOR FILING DATE: 1997-08-26
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 3018
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL SEQUENCE
 ; FEATURE:
 ; OTHER INFORMATION: VECTOR SEQUENCE: pGEM-T Easy Vector Plasmid Sequence
 US-09-486-142-7

Query Match 90.4%; Score 667; DB 5; Length 3018;
 Best Local Similarity 100.0%; Pred. No. 2.1e-184;
 Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 AGCTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTGTATAGTGT 131
 Db 129 agcttgagtattctatagtgctacacataatgctggttaataatgctggttt 188
 QY 132 CTTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACAGCGGGAAGCAAT 191
 Db 189 cctgtgtgaattgtttatccgctcacataatccacacatacagcggaagcataag 248
 QY 192 TGTAAAGCCTGGGTGCTTAAATGAGTGAAGTCACTAAATTTCCGCTTCCGCTCACTG 251
 Db 249 tgaagagcctgggtgcttaataatgagctcaacataatgctggttccgctcactg 308
 QY 252 CCGCTTTTCCAGCTCGGGAACCTGCTGCGCAAGTGCATTAATGAATCGGCAACGCCGCG 311
 Db 309 cccgctttccagctcggaacacctgctgcccagctgcttaataatgagtggtggtc 368
 QY 312 GGGAGAGCGGTTTGGGCTTATTTGGGCGCTTCTCCGCTTCCGCTCACTGCTGCGCG 371
 Db 369 gggagagcggtttgctgattggcgctctccgcttccgctcactgactgactgctg 428
 QY 372 TCGGTGCTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGCTTATCC 431
 Db 429 tcgggtcgctcggtcggtgagcggtatcagctcactcaaaagcggttaataatggttacc 488
 QY 432 ACAGAAATCAGGGGATTAACGAGCAAGAAACATGTGTAGCAAAAGGCCAGCAAAAGGCCAGG 491
 Db 489 acagaatcagggataaacgaggaagaacatgtgagcaaaagccagcaaaagggcag 548
 QY 492 AACCGTAAAGCGGCTTGGCGGTTTTCATAGGCTCCGCCCTCCGCTGACGAGCAT 551
 Db 549 aacccgtaaaagcggttgcgtggtttttccataggtcctccgctccgctccgctg 608
 QY 552 CACAAAATTCGAGCTCAAGTCAAGGTGGCGGAACCCCGAGAGCTATATAAGATACCA 611
 Db 609 cacaataatcagcgtcctcagtcagagtggtgcaaaacccgagagctataaagatacag 668
 QY 612 GCGTTTCCCCCTGGGAAGTCCCTCGTGGCGCTCTCTCTGTTCCGACCCCTGCCGCTTACCGGA 671

Db 430 acagaaacaggggataacagcaggaagaaacatgtgagcaaaagccagcaaaagccagg 489
QY 492 AACCGTAAAGAGCGCGTTCCTGGCGTTTTCATAGCTCCGCCCGCTGACGAGCAT 551
Db 490 aaccgtaaaaagccgcgttgcgttcttttccataggtccgccccctgacagcat 549
QY 552 CACAAAATCGAGCTCAAGTTCAGAGTGGCGAAACCGACAGGACTATAAGATACAG 611
Db 550 cacaataatcgagctcaagtcagagtgaggaaacccagacagactataaagataccag 609
QY 612 GCCTTTCCCGCTCGAAGCTCCCTGCGTCTCCTGCTTCGACCCCTGCGCTTACCGGA 671
Db 610 gegtctcccttggaagctccctgcgtctctctctctctctctctctctctctctct 669
QY 672 TACCTGTCGCCCTTCTCCCTTCGGGAAGCTGCGCTTCTCATAGCTACCGCTGAGG 731
Db 670 tacctgtccgccttctcccttccttccttccttccttccttccttccttccttcct 729
QY 732 TATCTCA 738
Db 730 tatctca 736

RESULT 5
PCT-US02-17451-7
; Sequence 7, Application PC/TUS0217451
; GENERAL INFORMATION:
; APPLICANT: CHROMOS MOLECULAR SYSTEMS, INC.
; APPLICANT: Perez, Carl
; APPLICANT: Fabijanski, Steven
; APPLICANT: Perkins, Edward
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation
; FILE OF INVENTION: Plant Artificial Chromosomes
; CURRENT APPLICATION NUMBER: PCT/US02/17451
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,687
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/296,329
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pGEMEasyNOS Plasmid
PCT-US02-17451-7

Query Match 90.4%; Score 667; DB 1; Length 3357;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 AGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAATCATGTCTAGCTGTTT 131
Db 70 agcttgagtattctatagtgatcactaaatagcttgcgtaatacatggtcatagctgtt 129
QY 132 CCTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACAGCGCGGAAGCAATAAG 191
Db 130 cctgtgtgaattgttattccgcctcacaaattccacaaatacagagcgggaagcataag 189
QY 192 TGTAAGCGCTGGGGTGCCTAATGAGTGAGTAACTACATTAATTTGGTTGCGCTCACTG 251
Db 190 tgaagcgtggggtgcctaaatgagtgagtaactacattattgcttgcgtcactg 249
QY 252 CCGGCTTTCCAGTCGGAACCTGTCGTCGACCTGCAATTAATGAATTCGGCCCAACGGCG 311
Db 250 ccgctcttcagtcgggaacctgtgtgcccagctgcattaa tgaatcgcccaacgcgcg 309
QY 312 GGGAGAGCGGTTTGGGTATGGGCGCTCTTCGCTTCTCGCTCACTGACTCGCTGCCG 371

Db 310 gggagaggcgtttgctgatttggcgctcttcgcttctcgtcactgactgctgctgc 369
QY 372 TCGGCTCGTTCGGCTCGGCGAGCGGTATCAGTCTCACTCAAGGCGGTAAATAGCGTTATCC 431
Db 370 tcggcgttcgctgctgagcggtatcagctcactcaagcggttaatacgtttatcc 429
QY 432 ACAGAAATCAGGGGATAAGCGAGGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG 491
Db 430 acagaatcagggataacgcaggaagaaca tggagcaaaagccagcaaaagccagg 489
QY 492 AACCGTAAAGAGCGCGCTTCGCTGCGTTTTCATAGCTCCGCCCGCTGACGAGCAT 551
Db 490 aaccgtaaaaagccgcgttgcgttcttttccataggtccgccccctgacagcat 549
QY 552 CACAAAATCAGCGCTCAAGTTCAGAGTGGCGAAACCGACAGGACTATAAGATACCGAG 611
Db 550 cacaataatcgagctcaagtcagagtgaggaaacccagacagactataaagataccag 609
QY 612 GCCTTTCCCGCTCGAAGCTTCCTGCTGCGTCTCCTGTTCCGACCCCTGCGCTTACCGGA 671
Db 610 gegtctcccttggaagctccctgcgtctctctctctctctctctctctctctctct 669
QY 672 TACCTGTCGCCCTTCTCCCTTCGGGAAGCTGCGCTTCTCATAGCTACCGCTGAGG 731
Db 670 tacctgtccgccttctcccttccttccttccttccttccttccttccttccttcct 729
QY 732 TATCTCA 738
Db 730 tatctca 736

RESULT 6
US-10-161-403-96
; Sequence 96, Application US/10161403
; GENERAL INFORMATION:
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pGEMEasyNOS Plasmid
US-10-161-403-96

Query Match 90.4%; Score 667; DB 7; Length 3357;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 72 AGCTTGAGTATCTATAGTGTCACTAAATAGCTTGGCGTAATCATGTCTAGCTGTTT 131
Db 70 agcttgagtattctatagtgatcactaaatagcttgcgtaatacatggtcatagctgtt 129
QY 132 CCTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACAGCGCGGAAGCAATAAG 191

Db	130	cctgtgtgaattgttatccgctcacaattccacacacatacagccggaagcataaag	189
QY	192	TGTAAGCCTGGGCTGCTTAATGAGTAACTACATTAATTTGGTTCGCTCACTG	251
Db	190	tgtaaagctgggtgcttaagtgtgagctactacataatcgcttgctcaactg	249
QY	252	CCGCTTTCCAGTTCGGGAACCTGTGTCAGCTGCATTAATGAATTCGGCCAAACGGCG	311
Db	250	cccgcttccagtcggaacacctgtgctcagctgcatlaaagaaatcgcccaacgcgcg	309
QY	312	GGAGAGCGGCTTGGCTATTTGGCGCTCTTCGCTTCCTCGCTCACTGCTCGCTCGC	371
Db	310	ggagagggcggttgctgattggcgctcttcgcttcctcgcctcactgactcgtcgcgc	369
QY	372	TGCGTTCGCTGCGGAGCGGCTATCAGCTCACTCAAGGCGGTAATACGCTTATCC	431
Db	370	tcggtcgctcgctcgagcggtatcagctcactcaaaagcggttaacggttatcc	429
QY	432	ACAGAAATCAGCGGATAACGAGGAAAGAACATGTGAGCAAAAGCCAGCAATACACG	491
Db	430	acagaaatcaggggataaacgaggaagacatgtgagcaaaagccagcaaaagggccag	489
QY	492	AACCGTAAAGGCGCGTTCGCTGCTTTCATAGCTCCGCGCCCTGACGAGCAT	551
Db	490	aacgtaaaagcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	549
QY	552	CACAAAATCAGCGGATAACGAGGAAAGAACATGTGAGCAAAAGCCAGCAATACACG	611
Db	550	cacaaaatcagcgctcaagtcagagtggtgcaaaacccgacaggaactataagataccag	609
QY	612	CGCTTCCCTGAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	671
Db	610	gcgttccctggaagctccctgctgctgctgctgctgctgctgctgctgctgctgctg	669
QY	672	TACCTGTCGCGCTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	731
Db	670	tacctgctgcttct	729
QY	732	TATCTCA 738	
Db	730	tatctca 736	
RESULT 7			
US-10-161-408-7			
; Sequence 7, Application US/10161408			
; GENERAL INFORMATION:			
; APPLICANT: Fabijanski, Steven			
; APPLICANT: Perkins, Edward			
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Preparation			
; FILE REFERENCE: 24601-419			
; CURRENT APPLICATION NUMBER: US/10/161,408			
; PRIOR FILING DATE: 2002-05-30			
; PRIOR FILING DATE: 2001-05-30			
; PRIOR FILING DATE: 2001-05-30			
; PRIOR FILING DATE: 2001-06-04			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 7			
; LENGTH: 3357			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: pGEMEasyNOS Plasmid			
US-10-161-408-7			
Query Match 90.4%; Score 667; DB 7; Length 3357;			
Best Local Similarity 100.0%; Pred. No. 2.1e-184;			
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY	72	AGCTTGAGTATTTCTATAGTGTACCTAAATAGCTTGGCTTAATCATGTGCTAGCTGTT	131
Db	70	agcttgagtagtctcatagctgacccctaaatagcttggtgagtaataatgctgctgctt	129
QY	132	CCTGTGTGAATTTGTTATTCGCTCAAAATCCACACATACGAGCCGGAAGCATTAAG	191
Db	130	cctgtgtgaattgttatccgctcacaattccacacacatacagcagccggaagcataaag	189
QY	192	TGTAAGCCTGGGCTGCTTAATGAGTAACTACATTAATTTGGTTCGCTCACTG	251
Db	190	tgtaaagctgggtgcttaagtgtgagctactacataatcgcttgctcactcgc	249
QY	252	CCGCTTTCCAGTTCGGGAACCTGTGTCAGCTGCATTAATGAATTCGGCCAAACGGCG	311
Db	250	cccgcttccagtcggaacacctgtgctcagctgcatlaaagaaatcgcccaacgcgcg	309
QY	312	GGAGAGCGGCTTGGCTATTTGGCGCTCTTCGCTTCCTCGCTCACTGCTCGCTCGC	371
Db	310	ggagagggcggttgctgattggcgctcttcgcttcctcgcctcactgactcgtcgcgc	369
QY	372	TGCGTTCGCTGCGGAGCGGCTATCAGCTCACTCAAGGCGGTAATACGCTTATCC	431
Db	370	tcggtcgctcgctcgagcggtatcagctcactcaaaagcggttaacggttatcc	429
QY	432	ACAGAAATCAGCGGATAACGAGGAAAGAACATGTGAGCAAAAGCCAGCAATACACG	491
Db	430	acagaaatcaggggataaacgaggaagacatgtgagcaaaagccagcaaaagggccag	489
QY	492	AACCGTAAAGGCGCGTTCGCTGCTTTCATAGCTCCGCGCCCTGACGAGCAT	551
Db	490	aacgtaaaagcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg	549
QY	552	CACAAAATCAGCGGATAACGAGGAAAGAACATGTGAGCAAAAGCCAGCAATACACG	611
Db	550	cacaaaatcagcgctcaagtcagagtggtgcaaaacccgacaggaactataagataccag	609
QY	612	CGCTTCCCTGAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	671
Db	610	gcgttccctggaagctccctgctgctgctgctgctgctgctgctgctgctgctgctg	669
QY	672	TACCTGTCGCGCTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC	731
Db	670	tacctgctgcttct	729
QY	732	TATCTCA 738	
Db	730	tatctca 736	
RESULT 8			
US-10-152-040-26			
; Sequence 26, Application US/10152040			
; GENERAL INFORMATION:			
; APPLICANT: ESCRIOU, NICOLAS			
; APPLICANT: VAN DER WERF, SYLVIE			
; APPLICANT: VIGNUZZI, MARCO			
; APPLICANT: GERBAUD, SYLVIE			
; TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS			
; TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS			
; FILE REFERENCE: 03495.0229-00000			
; CURRENT APPLICATION NUMBER: US/10/152,040			
; CURRENT FILING DATE: 2002-06-27			
; PRIOR APPLICATION NUMBER: 60/292,515			
; PRIOR FILING DATE: 2001-05-23			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 26			
; LENGTH: 8017			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: plasmid pm(DELTA)BB
US-10-152-040-26

Query Match 90.4%; Score 666.8; DB 7; Length 8017;
Best Local Similarity 97.9%; Pred. No. 3e-184;
Matches 687; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 40 GGGATCTCTAGAGTCGACCTGCGAGCATGCAAGCTTGTAGTATTTCTATAGTCTCACTTAA 99
DB 4836 gggatcctctagagtcgacctgaggcatgcaagcttcttcccttttagtgagggttaa 4895
QY 100 AT---AGCTTGGCGTAATCATGCTAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCA 156
DB 4896 ttccgagcttggcgttaataatggttcagctgttccctgtgtgaaattgttatccgctca 4955
QY 157 CAATTCCACACACATACGAGCGGAGCAATAAGTGTAAAGCTTGGGGTCCCTTAATGAG 216
DB 4956 caattccacacacatacagagcccggaagcaataagtgtaagcctggggtgcctaatgag 5015
QY 217 TGAGCTAACTCACATTAATTTGGCTGCTCACTGCCGCTTTTCCAGTCGGGAAACCTGT 276
DB 5016 tgagctaactcacattaattgctgtgctcaactgcccgtttccagtcgggaaacctgt 5075
QY 277 CGTGCCAGCTGCAATTAATGATGCGCAACGCGCGGGAGAGCGGTTTGGGTATTTGGGC 336
DB 5076 cgtgcagctgcaattaatgataatgcgcaacgcgcgggagagcggttgcgtattgggc 5135
QY 337 GCTCTCCGCTTCTCTCGCTCACTGACTGCTGGCTCGGCTCGGTTTCCAGTCGGGAGCGG 396
DB 5136 gctcttccgcttctctcgctcaactgactcgctgcgctcgcttgcgttcggtcgagcg 5195
QY 397 TATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGCAAGAA 456
DB 5196 tatcagctcactcaaaaggcgtaataacggttatccacagaaatcaggggataacgcagaa 5255
QY 457 AGAATATGTAGCAAAAGCGCCAGCAAAAGCGCCAGCAACCGTAAAGCGCGCTTGGTGG 516
DB 5256 agaatactgagcaaaaagccagcaaaaagccaggaacgtaaaaagccgcttgcgtgg 5315
QY 517 CGTTTTCATAGGCTCCGCGCCCTTGACGAGCATCACAAAATCAGCCTCAAGTCAGA 576
DB 5316 cgttttccatagggctccgcccccttgacgagcaatcacaaaaatcagcgtcaagtcca 5375
QY 577 GTGGCGAAACCCGACGAGCTATTAAGATACGAGCGTTTCCCGCTGGAAGCTCCCTCG 636
DB 5376 ggtggcgaacccgacaggaactataaagatacaggcggttccccctgggaagctccctcg 5435
QY 637 TCGCTCTCTCTTCCGACCTGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGG 696
DB 5436 tgcgctctctgttccgacctggcgcttaccggatacctgtccgcttctcccttcgg 5495
QY 697 GAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 738
DB 5496 gaagcgtggcgcttctcatagctcaactgtagtatctca 5537

RESULT 9

US-10-152-040-27
; Sequence 27, Application US/10152040
; GENERAL INFORMATION:
; APPLICANT: ESCRIOU, NICOLAS
; APPLICANT: VAN DER WERF, SYLVIE
; APPLICANT: VIGNUZZI, MARCO
; APPLICANT: GERBAUD, SYLVIE
; TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS
; TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS
; FILE REFERENCE: 03495, 0229-00000
; CURRENT APPLICATION NUMBER: US/10/152,040
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/292,515

; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27

LENGTH: 8092
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: plasmid pm(DELTA)FM
US-10-152-040-27

Query Match 90.4%; Score 666.8; DB 7; Length 8092;
Best Local Similarity 97.9%; Pred. No. 3e-184;
Matches 687; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 40 GGGATCTCTAGAGTCGACCTGCGAGCATGCAAGCTTGTAGTATTTCTATAGTCTCACTTAA 99
DB 4911 gggatcctctagagtcgacctgaggcatgcaagcttcttcccttttagtgagggttaa 4970
QY 100 AT---AGCTTGGCGTAATCATGCTAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCA 156
DB 4971 ttccgagcttggcgttaataatggttcagctgttccctgtgtgaaattgttatccgctca 5030
QY 157 CAATTCCACACACATACGAGCGGAGCAATAAGTGTAAAGCTTGGGGTCCCTTAATGAG 216
DB 5031 caattccacacacatacagagcccggaagcaataagtgtaagcctggggtgcctaatgag 5090
QY 217 TGAGCTAACTCACATTAATTTGGCTGCTCACTGCCGCTTTTCCAGTCGGGAAACCTGT 276
DB 5091 tgagctaactcacattaattgctgtgctcaactgcccgtttccagtcgggaaacctgt 5150
QY 277 CGTGCCAGCTGCAATTAATGATGCGCAACGCGCGGGAGAGCGGTTTGGGTATTTGGGC 336
DB 5151 cgtgcagctgcaattaatgataatgcgcaacgcgcgggagagcggttgcgtattgggc 5210
QY 337 GCTCTCCGCTTCTCTCGCTCACTGACTGCTGGCTCGGCTCGGTTTCCAGTCGGGAGCGG 396
DB 5211 gctcttccgcttctctcgctcaactgactcgctgcgctcggttcggttcggttcggttcg 5270
QY 397 TATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGCAAGAA 456
DB 5271 tatcagctcactcaaaaggcggttaatacgggttatccacagaaatcaggggataacgcagaa 5330
QY 457 AGAATATGTAGCAAAAGCGCCAGCAAAAGCGCCAGCAACCGTAAAGCGCGCTTGGTGG 516
DB 5331 agaatactgagcaaaaagccagcaaaaagccaggaacgtaaaaagccgcttgcgtgg 5390
QY 517 CGTTTTCATAGGCTCCGCGCCCTTGACGAGCATCACAAAATCAGCCTCAAGTCAGA 576
DB 5391 cgttttccatagggctccgcccccttgacgagcaatcacaaaaatcagacgtcaagtcca 5450
QY 577 GTGGCGAAACCCGACGAGCTATTAAGATACGAGCGTTTCCCGCTGGAAGCTCCCTCG 636
DB 5451 ggtggcgaacccgacaggaactataaagatacaggcggttccccctgggaagctccctcg 5510
QY 637 TCGCTCTCTCTTCCGACCTGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGG 696
DB 5511 tgcgctctctgttccgacctggcgcttaccggatacctgtccgcttctcccttcgg 5570
QY 697 GAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA 738
DB 5571 gaagcgtggcgcttctcatagctcaactgtagtatctca 5612

RESULT 10

US-10-152-040-28
; Sequence 28, Application US/10152040
; GENERAL INFORMATION:
; APPLICANT: ESCRIOU, NICOLAS
; APPLICANT: VAN DER WERF, SYLVIE
; APPLICANT: VIGNUZZI, MARCO

```

APPLICANT: GERBAUD, SYLVIE
TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS
TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 03495.0229-00000
CURRENT APPLICATION NUMBER: US/10/152,040
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/292,515
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 10417
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: plasmid pM(Delta)BB-GFP-IcmvNP
US-10-152-040-28

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RESULT 11
; US-09-813-453A-72
; Sequence 72. Application US/09813453A
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Paterson, Thomas A.
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OG2-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 6688
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid, pAN336
; US-09-813-453A-72

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Db 4581 acctgccgttacggatacactgtccgccttctcccttcgggaagcgtggcgcttctc 4640

QY 714 CATAGCTCACGCTGTAGGTATCTCA 738
|||||

Db 4641 catagctcacgctgtaggatctca 4665

RESULT 12

```

PCT-US02-21336-27
; Sequence 27, Application PC/TUS0221336
; GENERAL INFORMATION:
; APPLICANT: OmniGene BioProducts, Inc. et al.
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGT-154PC
; CURRENT APPLICATION NUMBER: PCT/US02/21336
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4606
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
PCT-US02-21336-27

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Query Match									
Best Local Similarity 90.2%; Score 665.4; DB 1; Length 4606;									
Matches 666; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	72	AGCTTGAGTATTCATATAGTGTCACCTAAATAGCTTGCGCTAAATCATCATGTCATACCTGTTT	131						
Db	1917	agcttgagttattctatagtgtaactaaatagcttgcgtaatacaggtcatagcgttt	1976						
QY	132	CCGTGTGAAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCGCGGAACATAAAG	191						
Db	1977	ccgtgtgaaatgtttatccgtccacaattcccacaacatacgccggaagcataaag	2036						
QY	192	TGTAAAGCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTCGCTTGCCTCACATG	251						
Db	2037	tgtaaagcctgggggtgccaataagtgtagctaaactcacattaatgctgttgcgctcactcg	2096						
QY	252	CCGCTTTCCAGTCGCGGAAACCTGTCTGTCAGCTGCATTAATGAATCGGCCAACGCGCG	311						
Db	2097	ccgcgtttccagtcgggaaacctgctgcaagctgcattaatgaatcgcccaacgcgcg	2156						
QY	312	GGGAGAGCGGTTTTCGCTATTCGGGCGCTCTTCCGCTTCTCTGCTCACTGACTCGCTGCGC	371						
Db	2157	gggaagagcggtttgcgattg99gcgtcttcggtctcgtctcactgactcgctgcgcg	2216						
QY	372	TCGGTTCGTTTCGGCTCGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGTTATPC	431						
Db	2217	tcggtcggtcgtcgctcg9cg9agc9gatacgcactcaaa99c99taatcgttatcc	2276						
QY	432	ACAAATCAGGGGATAACGCAAGGAAGACATGTGAGCAAAAGCCACGAAAGCCACGG	491						
Db	2277	acagaatcagg9gataacgc9g9aagaaacatagtgagcaaa9ccagcaaa9ccag9	2336						
QY	492	AACCGTAAAGGCCGGTTCGTGGCGTTTTCATAGGCTCGGCCCTCTGACGAGCAT	551						
Db	2337	aaccgtaaa9gc9c9gttgc9gcttttcgataggctcgc9cccccctgacgagcat	2396						
QY	552	CACAAATCGAGCTCAAGCTCAGAGTGCGGGAACCCGACAGGACTATAAAGATACCCAG	611						
b	2397	cacaaaatcgcgcctcaagtcag9gt9gc9aaaccc9acaggactataaagataccag	2456						
QY	612	GCCTTTCCCGCTGAGCTCCCTGTCGCGCTCTCTCTGTTCCGAGCCCTGCGGCTACCGGA	671						
b	2457	gcggttccccctt9gaagctccctcgtagcgtctcctgttccgaacctgcgcctaccg9a	2516						
QY	672	TACCTGTCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTACGCTGTAGG	731						

Db 2517 taactgcgccttctccctcgggaagcggcgcttctcatagctcacgctgagg 2576
 QY 732 TATCTCA 738
 Db 2577 tattctca 2583

RESULT 13

```

RESULT 13
PCT-US02-21336-30
; Sequence 30, Application PC/TUS0221336
; GENERAL INFORMATION:
; APPLICANT: OmniGene Bioproducts, Inc. et al.
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154PC
; CURRENT APPLICATION NUMBER: PCT/US02/21336
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 5983
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
PCT-US02-21336-30

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Query Match	90.2%	Score 665.4	DB 1	Length 5983
Best Local Similarity 99.9%	Pred. No. 7.1e-184			
Matches 666	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 72	ACGTTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAAATCATATGGTCATAGCTGTTT	131		
Db 3294	agcttgagattctatagtcaccataatagcttggttaatcatcgttcatacgttc	3353		
QY 132	CCTGTGTCAAATGTTATCCGGTCAAAATTCACACAAACATACGAGCCGGAAGCATAAAG	191		
Db 3354	cctgtgaaattgtaaccgtctcaattccacaacaatacagcagcggaagcataaag	3413		
QY 192	TGTAAGCCTGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGGTTGGCTCACTG	251		
Db 3414	tgtaaagcctggggtgcctaatagtgagctaaactcaattatctgcgttcactg	3473		
QY 252	CCGCTTTTCAGTCGGGAAACCTCTGCTGCCAGCTGCATTAAATGCGCAACGCGCG	311		
Db 3474	cccgcttccagtcgggaaacctgctggcagctgattaatgaatcggccaacgcgcg	3533		
QY 312	GGCAGAGGCGGTTTGGCTATTGGCGCTCTTCGCTTCCTCGCTCACTGCTCGCTCGCG	371		
Db 3534	gggaagggcggtttgcgtatctgggcgtcttcgcttcctcgctcactgcgtgcgcg	3593		
QY 372	TCGGTCGTCGGTCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTAAATACGGTTATCC	431		
Db 3594	tcggttcgttcggtgcgcgcgcggtatcagctcaactcaaaaggcggtaacggttatcc	3653		
QY 432	ACAGAAATCAGGGATAAACGACGAAAGACATGTGACCAAAAGCCAGCAAAAGGCCAGG	491		
Db 3654	acagaatcaggggataaacgcagaaagaacatcgtgacaaaggccagcaaaaggccag	3713		
QY 492	AACCGTAAAAAGCCGCTTGTGGGTTTTTCCTATAGCTCCGCCCCCTGACGAGCAT	551		
Db 3714	aacgtaaaaagccgcgtgcgtgcgttttcgtagcgtcgcgcctgaacgagcat	3773		
QY 552	CACAAAAATCGACGCTCAAGTCAGAGGTGGCCAAACCCGACAGGACTATAAAGATACCG	611		
Db 3774	cacaaaaatcgacgtcaagtacagaggctgggaacccgacaggaactataaagaatacag	3833		
QY 612	GCGTTTCCCCCTGGAAGCTCCCTGTCGGCTCTCCTGTTCCGACCCCTGCCGCTTACCGA	671		
Db 3834	gcggttccccctggaaagctccctgcgtctcctgcttcgcgaacctgcgcttacgga	3893		

Thu Aug 1 12:08:50 2002

Db 6111 cacaataatcgacgctcaagtcagagggtg99gaacccgacagagactataagataccag 6170
 QY 612 GGGTTTCCCTCGGAGGCTCCCTCGTGGCTCTCTGTTCCAGCTGCCGCTTACCGA 671
 Db 6171 gcggttccccctcggaagctccctcgctctctctgcttccgacccctgcttcccgga 6230
 QY 672 TACCTGTCCGCTTCTCTCCCTCGGAGGCTGGGCTTCTCATAGCTCAGCTGTAGG 731
 Db 6231 tacctgtccgcttctcccttcggaagcgtg99cgcttctcatagctcagcgttagg 6290
 QY 732 TATCTCA 738
 Db 6291 tatctca 6297

RESULT 15
 PCT-US02-17452-32
 ; Sequence 32, Application PC/TUS0217452
 ; GENERAL INFORMATION:
 ; APPLICANT: CHROMOS MOLECULAR SYSTEMS, INC.
 ; APPLICANT: Perkins, Edward
 ; APPLICANT: Perez, Carl
 ; APPLICANT: Lindenbaum, Michael
 ; APPLICANT: Greene, Amy
 ; APPLICANT: Leung, Josephine
 ; APPLICANT: Fleming, Elena
 ; APPLICANT: Stewart, Sandra
 ; APPLICANT: Shellard, Joan
 ; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
 ; FILE REFERENCE: 24601-420PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/17452
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/294,758
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: 60/366,891
 ; PRIOR FILING DATE: 2002-03-21
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 2713
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: pNEB193 plasmid
 PCT-US02-17452-32

Query Match 87.5%; Score 645.8; DB 1; Length 2713;
 Best Local Similarity 94.5%; Pred. No. 3.1e-178;
 Matches 681; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 18 GCGAATTCGAGCTCCGCTACCGGGGATCCTCTAGAGTCGACTCGAGCATGCAAGCTTG 77
 Db 394 gTgaattcgagctcggtaccggggcgccggatccttaataag---tctagagctg 450
 QY 78 AGTATTCTATAGTCACCTTAATAGCTGGCTAATCATGTGTATGTCTGTCTGTG 137
 Db 451 actgtttaacctcgaggcatgcaagcttggcgttaataatgctatagctgttctg 510
 QY 138 TGAATTTGTTATCCGCTCACAAATTCACACAAATACAGCGCGGAGCAATAGCTGATAA 197
 Db 511 tgaattgtttatccgtctcaaatccacacacatacagcgcggaagcataaagtgtaa 570
 QY 198 GCCTGGGTGCTTAATAGTCAGCTAACCTAACCTAACCTAACCTAACCTAACCTAACCT 257
 Db 571 gcttgggtgcttaataagtgagctaacctaacctaacctaacctaacctaacctaacct 630
 QY 258 TTCAGTCGGAACCTGTCTGCTCCAGCTCATTAATGAATGCGGCACACCGCGGGGAGA 317
 Db 631 ttcagtcgggaacctgctgctccagctgcaatgaatgaatgaatgaatgaatgaatgaat 690
 QY 318 GCGGTTTGGCTATTGGCGCTCTTCCGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTC 377

QY 672 TACCTGTCCGCTTCTCTCCCTCGGAGGCTGGGCTTCTCATAGCTCAGCTGTAGG 731
 Db 3894 tacctgtccgcttctcccttcggaagcgtg99cgcttctcatagctcagcgttagg 3953
 QY 732 TATCTCA 738
 Db 3954 tatctca 3960

RESULT 14
 US-09-813-453A-71
 ; Sequence 71, Application US/09813453A
 ; GENERAL INFORMATION:
 ; APPLICANT: Yocum, R. Rogers
 ; APPLICANT: Patterson, Thomas A.
 ; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
 ; TITLE OF INVENTION: ANTIBIOTICS
 ; FILE REFERENCE: OG2-001
 ; CURRENT APPLICATION NUMBER: US/09/813,453A
 ; CURRENT FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: US 60/227,860
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 09/667,569
 ; PRIOR FILING DATE: 2000-09-21
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 71
 ; LENGTH: 8320
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid, PAN296
 US-09-813-453A-71

Query Match 90.2%; Score 665.4; DB 5; Length 8320;
 Best Local Similarity 99.9%; Pred. No. 7.7e-184;
 Matches 666; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 AGCTGTAGTATCTATAGTGTACCTAAATAGCTTGGCTAATCATGTGTATAGCTGTGT 131
 Db 5631 agcttgatattctatagtgcaactaaatagcttggttaataatgctatagctgtt 5690
 QY 132 CCGTGTGAAATTTGTTATCCGCTCACAAATTCACACACATACAGCGGAGGATAAG 191
 Db 5691 cctgtgtgaattgtatccgctcaaatccacacacatacagcgcggaagcataaag 5750
 QY 192 TGTAAAGCTGGGTGCTTAATAGCTAGCTAACCTAACCTAACCTAACCTAACCTAACCT 251
 Db 5751 tgtaaagcctgggtgctcaatgagctgaactcaacttaattgctgctcactg 5810
 QY 252 CCGCTTTTCAGTCGGGAAACCTGTGCTGCCAGCTGCATTAATGAATCGCCAAACGCGG 311
 Db 5811 ccgctttccagtcgggaacctgctgcccagctgcatatgaatgacgcaacgcgcg 5870
 QY 312 GGAGAGCGGTTGGGTATTGGCGCTTTCGCTTTCGCTCACTGCTGCTGCTGCTGCTG 371
 Db 5871 gggagagcggttgagttggttggcgcttccgcttccgcttccgcttccgcttccgct 5930
 QY 372 TCGGTGCTTGGCTGCGGCGAGGGGTATCAGCTCACTCAAGCGGTTATACGCTTATCC 431
 Db 5931 tcggtgcttggctgcgagcgggtatcagctcaactcaagcgggttaaactggttatcc 5990
 QY 432 ACAGAAATCAGGGATACCGAGGAAAGCAATGTGAGCAAAAGCCAGCAAAAGGCGCAGG 491
 Db 5991 acagaaatcagggataacgcgaggaagataatgtgagcaaaagccagcaaaagcagc 6050
 QY 492 AACCGTAAAAAGCGCGCTTCTGCGCTTTTCCATAGCTCCCGCCCTGACGAGCAT 551
 Db 6051 aaccgtaaaaagcgctgtgctggttctgagaggttctgagaggttctgagaggttctgagag 6110
 QY 552 CACAAAAATCCAGCTCAAGTCAGAGTGGGCAACCGGACAGGACTATAAGATACGAG 611

Db 691 ggcgggttgctgattggcgctcttcgcgttcctcgtcactgactgctgcgtcgcgtc 750
 QY 378 GTTCGGCTGCGCGAGCGGTATCAGCTCAACAGGGGTAAACGGTTATCCACAGAA 437
 Db 751 gtteggctgcggcgagcggtatcagctcactcaaaaggcggtacacggttatccacagaa 810
 QY 438 TCAGGGGATAACCGAGGNAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGT 497
 Db 811 tcaggggataaacgcaggaagaacatgtgagcaaaagccagcaaaagccaggaaccgt 870
 QY 498 AAAAGGCCGCTTGTGGGTGTTTTCATAGGCTCCGCCCTGACGAGCATCACAAA 557
 Db 871 aaaaagccgcgttgctggcggttttccataggtccgcgccctgacgagcatcacaaa 930
 QY 558 AATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTWT 617
 Db 931 aatcgacgtccaagtcagaggtggcgaaccgcgagactataaagataaccagggcgtt 990
 QY 618 CCCCTGGAGAGTCCCTCGCTCTGCTGTTCGACCGCTGCCGCTTACCGGATACCTG 677
 Db 991 cccctggagctccctcgtcgtctcctgttccgacctgcccgtaccggataccctg 1050
 QY 678 TCCGCTTCTCCCTTCGCGAAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTC 737
 Db 1051 tcgccttctccctccggagcggtggcgcttctctcatagctcacgctgtaggtatctc 1110
 QY 738 A 738
 Db 1111 a 1111

Search completed: August 1, 2002, 11:05:27
 Job time: 8722 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 1, 2002, 07:39:54 ; Search time 2881.61 Seconds
(without alignments)
8837.974 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCACGTCATGCTGCTGCA.....GGACATTCCTGCCAACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0 *
Searched: 1797656 seqs, 10463268293 residues 3595312

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
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- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description

1	1217	100.0	1217	6	AR036903	Sequence
2	1217	100.0	1217	6	AR141142	Sequence
3	1215.4	99.9	7249	12	M13MP18	X02513 Cloning vec
4	1215.4	99.9	7250	12	SYNMI3M18V	M77815 M13mp18 pha
5	1201.2	98.7	64372	2	HSLUCA6	Z84493 Homo sapien
6	1184.8	97.4	7244	12	SYNMI3M10V	L08819 M13mp10 pha
7	1165.2	95.7	9955	6	I08051	I08051 Sequence 7
8	1161.4	95.4	7196	12	SYNMI3MP2V	L08818 M13mp2 phag
9	1161.4	95.4	7229	12	SYNMI3MP8V	M77826 M13mp8 phag
10	1161.4	95.4	7232	12	SYNMI3MP8V	M77826 M13mp8 phag
11	1161.4	95.4	7232	12	SYNMI3MP8V	M77826 M13mp8 phag
12	1161.4	95.4	7232	12	SYNMI3MP8V	M77826 M13mp8 phag
13	1161.4	95.4	7232	12	SYNMI3MP8V	M77826 M13mp8 phag
14	1159.8	95.3	7196	12	SYNMI3MP1V	L08833 M13mp1 pha
15	1156.8	95.1	7265	12	SYNMI3MP1V	L08833 M13mp1 pha
16	1156.4	95.0	7244	12	SYNMI3MP1V	L08820 M13mp1 pha
17	1156.4	95.0	7250	12	SYNMI3MP1V	L08820 M13mp1 pha
18	1150.8	94.6	7294	6	AR161799	L08874 PhageScript
19	1150.8	94.6	7294	6	AR161799	L08874 PhageScript
20	1150.8	94.6	7294	6	AR161799	L08874 PhageScript
21	1140.4	93.0	7083	6	AR131047	AR161803 Sequence
22	1131.4	93.0	7317	6	AR035975	AR131047 Sequence
23	1131.4	93.0	7317	6	AR035975	AR131047 Sequence
24	1131.4	93.0	7320	6	AR161800	AR161800 Sequence
25	1131.4	93.0	7557	6	AR035977	AR035977 Sequence
26	1131.4	93.0	7557	6	AR035977	AR035977 Sequence
27	1131.4	93.0	8118	6	AR035978	AR035978 Sequence
28	1131.4	93.0	8118	6	AR035978	AR035978 Sequence
29	1131	92.9	7394	6	AR161804	AR161804 Sequence
30	1131	92.9	7409	6	AR161802	AR161802 Sequence
31	1131	92.9	7445	6	AR035974	AR035974 Sequence
32	1131	92.9	7445	6	AR035974	AR035974 Sequence
33	1131	92.9	7445	6	AR161801	AR161801 Sequence
34	1131	92.9	7445	6	AR161801	AR161801 Sequence
35	1131	92.9	7729	6	AR035976	AR035976 Sequence
36	931.2	76.5	9472	6	AX287808	AX287808 Sequence
37	927.4	76.2	7599	12	SYNMI3MP9V	M77827 M13mp9 phag
38	927.4	76.2	7599	12	SYNMI3MP9V	M77827 M13mp9 phag
39	877	72.1	2000	6	I01987	I01987 Sequence 7
40	835.6	68.7	151477	2	AC021926	AC021926 Homo sapi
41	821.8	67.5	120538	2	AC015768	AC015768 Homo sapi
42	803.4	66.0	77945	2	AC022837	AC022837 Homo sapi
43	795	65.3	6407	7	INM13X	V00604 Phage M13 g
44	794.2	65.3	173561	2	AC016809	AC016809 Homo sapi
45	793.6	65.2	131156	2	AC015934	AC015934 Homo sapi

ALIGNMENTS

RESULT	1	AR036903	Sequence	1 from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR036903	Sequence	1 from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
DEFINITION	AR036903	Sequence	1 from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
ACCESSION	AR036903	Sequence	1 from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
VERSION	AR036903.1	GI:5954759						
KEYWORDS		Unknown.						
SOURCE		Unknown.						
ORGANISM		Unclassified.						
REFERENCE		1 (bases 1 to 1217)						
AUTHORS		Lee, L.G., Spurgeon, S.L. and Rosenblum, B.						
TITLE		Energy transfer dyes with enhanced fluorescence						
JOURNAL		Patent: US 5800996-A 1 01-SEP-1998;						
FEATURES		location/Qualifiers						
source		1. .1217						
BASE COUNT		335 a 291 c 321 g 270 t						
ORIGIN								

Query Match 100.0%; Score 1217; DB 6; Length 1217;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 CATACAGCGCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATAGTGAAGCTAACTAC 180

Qy 181 ATTAATTCGGTTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 240
Db 181 ATTAATTCGGTTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 240

Qy 241 TTAATGAATTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 300
Db 241 TTAATGAATTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 300

Qy 301 TTTCTTTTCCAGTGCAGCGGCAACAGCTGATTTGCCCTTTCCAGTCCGGCTGCCCTGAG 360
Db 301 TTTCTTTTCCAGTGCAGCGGCAACAGCTGATTTGCCCTTTCCAGTCCGGCTGCCCTGAG 360

Qy 361 GTTGCAAGCGGCTCCAGCTGTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 420
Db 361 GTTGCAAGCGGCTCCAGCTGTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 420

Qy 421 TTTCCGAATTCGGCAAAATCCCTTATAAATCAAAAGTAAAGTAAAGTAAAGTAAAGT 480
Db 421 TTTCCGAATTCGGCAAAATCCCTTATAAATCAAAAGTAAAGTAAAGTAAAGTAAAGT 480

Qy 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAAGAACCTGGACTCCACGTCMAAGGGCG 540
Db 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAAGAACCTGGACTCCACGTCMAAGGGCG 540

Qy 541 AAAAACCCTCTATCAGGCGGATGCCCACTACGTGAACCATCACCCCAATCAAGTTT 600
Db 541 AAAAACCCTCTATCAGGCGGATGCCCACTACGTGAACCATCACCCCAATCAAGTTT 600

Qy 601 GGGGTCCAGTGCCTGTAAGCACTAAATCGAACCTTAAGGGAGCCCGGCTTATAGC 660
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Qy 661 TTGACGGGAAAGCCGCGAAGTGGCGAGAAAGGAGAAAGGAGAAAGGAGGAGCGGG 720
Db 661 TTGACGGGAAAGCCGCGAAGTGGCGAGAAAGGAGAAAGGAGAAAGGAGGAGCGGG 720

Qy 721 CGCTAGGCGCTGGCAGTGTACGGTCAAGTGTAGCGTCAAGTGTAGCGTCAAGTGTAG 780
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Qy 841 CCTGCTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGAGTATTAAGCAGGA 900
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Qy 901 ACGGTACGCGAGTCTTTCAGAGTGTGTTTATATCATGAGGCGCAGGCTAAAGAG 960
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Qy 1021 TTGCTGAGTGAAGAGTCAAACTATCGGCTTGCCTGATATATCCAGAACATATTAC 1080
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Qy 1141 TCTGAAATGGATTTATTTACATTTGGCAGATTCACAGTCCACAGTCAATATAAGGGA 1200
Db 1141 TCTGAAATGGATTTATTTACATTTGGCAGATTCACAGTCCACAGTCAATATAAGGGA 1200

Qy 1201 CATTTGGCCCAACAGAG 1217
Db 1201 CATTTGGCCCAACAGAG 1217

RESULT 2
AR141142
LOCUS AR141142
DEFINITION Sequence 1 from patent US 6145434.
ACCESSION AR141142
VERSION AR141142.1 GI:15100659
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1217)
AUTHORS Tanaka,T. and Kobayashi,K.
TITLE Stencil printing method and device
JOURNAL Patent: US 6145434-A 1 14-NOV-2000;
FEATURES
source
location/Qualifiers
1. 1217
BASE COUNT 335 a 291 c 321 g 270 t
ORIGIN

Query Match 100.0%; Score 1217; DB 6; Length 1217;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCAAGCTTGCATGCGCTGCGAGTCCAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
Db 1 GCCAAGCTTGCATGCGCTGCGAGTCCAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60

Qy 61 GTAATCATGTGTCATAGCTGTTCTCTGTGTAAGATTTATCCGGTTCACAAATTCACACAA 120
Db 61 GTAATCATGTGTCATAGCTGTTCTCTGTGTAAGATTTATCCGGTTCACAAATTCACACAA 120

Qy 121 CATACAGCGCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATAGTGAAGCTAACTAC 180
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Qy 181 ATTAATTCGGTTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 240
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Qy 241 TTAATGAATTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 300
Db 241 TTAATGAATTCGGCTCACTGCCCTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 300

Qy 301 TTTCTTTTCCAGTGCAGCGGCAACAGCTGATTTGCCCTTTCCAGTCCGGCTGCCCTGAG 360
Db 301 TTTCTTTTCCAGTGCAGCGGCAACAGCTGATTTGCCCTTTCCAGTCCGGCTGCCCTGAG 360

Qy 361 GTTGCAAGCGGCTCCAGCTGTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 420
Db 361 GTTGCAAGCGGCTCCAGCTGTTTCCAGTCCGGGAACCTGTCTGCCAGTGC 420

Qy 421 TTTCCGAATTCGGCAAAATCCCTTATAAATCAAAAGTAAAGTAAAGTAAAGTAAAGT 480
Db 421 TTTCCGAATTCGGCAAAATCCCTTATAAATCAAAAGTAAAGTAAAGTAAAGTAAAGT 480

Qy 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAAGAACCTGGACTCCACGTCMAAGGGCG 540
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BASE COUNT	1768 a	1538 c	1533 g	2410 t
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Query Match	99.9%; Score 1215.4; DB 12; Length 7249;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 1216; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	GCCAAAGCTTCGATGCTGCGAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTC	60	
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QY	61	GTAATCATGTGTCATAGCTGTTTCCGTGTGAAATTTGTTATCCGCTCAATTCACACAA	120	
Db	6229	GTAATCATGTGTCATAGCTGTTTCCGTGTGAAATTTGTTATCCGCTCAATTCACACAA	6170	
QY	121	CATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTAC	180	
Db	6169	CATACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAGCTAACTAC	6110	
QY	181	ATTAATTCGCTTGCCTCACTGCCGCTTTCAGTCCGGGAAACCTGTCTGCGAGTGCA	240	
Db	6109	ATTAATTCGCTTGCCTCACTGCCGCTTTCAGTCCGGGAAACCTGTCTGCGAGTGCA	6050	
QY	241	TTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGCGCCAGGGTGGTTT	300	
Db	6049	TTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGCGCCAGGGTGGTTT	5990	
QY	301	TTCTTTTTCACAGTCAGAGCGGCAACAGCTGATTTGCCCTTCACCGCTGGCCCTGAGAGA	360	
Db	5989	TTCTTTTTCACAGTCAGAGCGGCAACAGCTGATTTGCCCTTCACCGCTGGCCCTGAGAGA	5930	
QY	361	GTTCGAGCAAGCGGCTCCAGCTGGTTTGCCTCCAGCAGCGGAAATCCTGTTGATGGTGG	420	
Db	5929	GTTCGAGCAAGCGGCTCCAGCTGGTTTGCCTCCAGCAGCGGAAATCCTGTTGATGGTGG	5870	
QY	421	TTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGT	480	
Db	5869	TTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGT	5810	
QY	481	TGTTCCAGTTTGGCAACAGAGTCCACTATTTAAAGAACGTGAGCTCCAAAGGGCG	540	
Db	5809	TGTTCCAGTTTGGCAACAGAGTCCACTATTTAAAGAACGTGAGCTCCAAAGGGCG	5750	
QY	541	AAAAACCGTCTATCAGGGGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTT	600	
Db	5749	AAAAACCGTCTATCAGGGGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTT	5690	
QY	601	GGGTGCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGGAGCCCGGATTTAGAGC	660	
Db	5689	GGGTGCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGGAGCCCGGATTTAGAGC	5630	
QY	661	TTGACGGGAAAGCCGCGAACGTGGCGAGAAAGGAGGAAAGGAGGAGGGG	720	
Db	5629	TTGACGGGAAAGCCGCGAACGTGGCGAGAAAGGAGGAAAGGAGGAGGGG	5570	
QY	721	CGGTAGGGCTTGGCAAGTGTAGCGGTACCGCTGCGGTACACACCGCCGCGCT	780	
Db	5569	CGGTAGGGCTTGGCAAGTGTAGCGGTACCGCTGCGGTACACACCGCCGCGCT	5510	
QY	781	TAATGCGCCGTACAGGGCGGTACTATGTTTGTCTTTCAGCAGCACGATTAACGTCGTTT	840	
Db	5509	TAATGCGCCGTACAGGGCGGTACTATGTTTGTCTTTCAGCAGCACGATTAACGTCGTTT	5450	
QY	841	CCTGTTTGGAAATCAGAGCGGAGTAAACAGGAGCGCGATTAAGGGATTTTAGACAGA	900	
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Db	541	AAAAACCGTCTATCAGGGGATGGCCACTACGTGAACCATCACCCAAAATCAAGTTTTT	600	
QY	601	GGGTGCGAGTGCCTTAAAGCACTAAATCGGAACCCCTAAAGGAGCCCGGATTTAGAGC	660	
Db	601	GGGTGCGAGTGCCTTAAAGCACTAAATCGGAACCCCTAAAGGAGCCCGGATTTAGAGC	660	
QY	661	TTGACGGGAAAGCCGCGAACGTGGCGAGAAAGGAGGAAAGGAGGAGCGGG	720	
Db	661	TTGACGGGAAAGCCGCGAACGTGGCGAGAAAGGAGGAAAGGAGGAGCGGG	720	
QY	721	CGGTAGGGCTTGGCAAGTGTAGCGTCACTGCTTTCAGCAGCACGATTAACGTCGTTT	780	
Db	721	CGGTAGGGCTTGGCAAGTGTAGCGTCACTGCTTTCAGCAGCACGATTAACGTCGTTT	780	
QY	781	TAATGCGCCGTACAGGGCGGTACTATGTTTGTCTTTCAGCAGCACGATTAACGTCGTTT	840	
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QY	841	CCTGTTTGGAAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTTAGACAGA	900	
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QY	961	TCTGTCCATCAGCAAAATTAACCGTTGTAGCAATACCTTCTTTGATAGTAATACATCAC	1020	
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QY	1021	TTGCTGAGTAGAAGAACTCAAACTATCGGCTTTCGCTGGTGAATATCCAGAAATATPAC	1080	
Db	1021	TTGCTGAGTAGAAGAACTCAAACTATCGGCTTTCGCTGGTGAATATCCAGAAATATPAC	1080	
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QY	1141	TCTGAATGGATTTATACATTGGCAGATTCCACGAGTCCACGACGACGATTAAGAGGA	1200	
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QY	1201	CATTCTGCGCAACAGAG 1217		
Db	1201	CATTCTGCGCAACAGAG 1217		
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M13MP18/c				
LOCUS	M13MP18	7249 bp	DNA	linear SYN 30-JAN-2002
DEFINITION	Cloning vector M13mp18.			
ACCESSION	X02513			
VERSION	X02513.1 GI:58253			
KEYWORDS	cloning vector.			
SOURCE	Cloning vector M13mp18.			
ORGANISM	artificial sequence; vectors.			
REFERENCE	1. (bases 1 to 7249)			
AUTHORS	Yanisch-Perron,C., Vieira,J. and Messing,J.			
TITLE	Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors			
JOURNAL	Gene 33 (1), 103-119 (1985)			
MEDLINE	85180545			
FEATURES	Location/Qualifiers			
source	1..7249			
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	/db_xref="taxon:31778"			
misc_feature	1..7249			
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Db 5269 TTGCCTGAGTAGAAGAACTCAAACTATCGGCCTTGTGTGTAATATCCAGAACAAATATTAC 5210
QY 1081 CCCCAGCCATTGCAACAGCAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCG 1140
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QY 1141 TCTGAATGGATATTATACATTGGCAGATTACACAGTTCACACACAGCAATATAAGGGA 1200
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QY 1201 CATTCTGGCCACACAG 1217
Db 5089 CATTCTGGCCACACAG 5073

RESULT 4
SYNML3M18V/c
LOCUS SYNML3M18V 7250 bp DNA circular SYN 01-OCT-1993
DEFINITION M13mp18 phage cloning vector.
ACCESSION M77815
VERSION M77815.1 GI:208802
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Synthetic construct DNA.
artificial construct
1 (bases 1 to 7250)
Gilbert, W.
Obtained from VecBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program.

TITLE M13mp18 - Phage cloning vector
DATE 03-FEB-1986
#sequence 02-APR-1986
ACCESSION V80018
SOURCE artificial
REFERENCE
#number 1
#authors Norrander J., Kempe T., Messing J.
#Journal Gene (1983), 26: 101-106
#number 2
#authors Yanisch-Perron C., Vieira J., Messing J.
#Journal Gene (1985) 33: 103-119
#comment shows the complete compiled sequence
REFERENCE
#number 3
#authors Dotto G.P., Zinder N.D.
#Journal Nature (1984) 311: 279-280
#comment mutation: T at pos 6968, G at pos 6125 in M13 wildtype
REFERENCE
#number 4
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-v-1
COMMENT
Obtained 3-MAR-1986 from J. Messing, Waksman Institute, NJ on
floppy disc
Revised 02-APR-1986 by F. Pfeiffer, MPI, Martinsried
pos 898 TTT instead of TT to restore the gene v reading frame
KEYWORDS
CROSSREFERENCE
#prerevised
#parent
GenBank(50):M11454, EMBL(11):M13mp18
#parent
VecBase(3):M13mp10
#parent

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GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bGal18
#brother
VecBase(3):M13mp19
#offspring
VecBase(3):pUC18
PARENT
Features of M13mp18 (7250 bp)
residue source
1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6287 1- 57 M13mp18/pUC18-Polylinker
6290-6711 1303-1724 Lac-Operon
6712-7250 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp18 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6522 G T 1535 Lac
mut 6938 T C 6095 phage M13
mut 6968 T G 6125 phage M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
it was changed to TTT to restore the reading frame of gene v.
M13mp18 does not contain amber mutations in gene I and gene II.
FEATURE
POLYLINKER EcoRI-SacI-KpnI-SmaI-BamHI-XbaI-SalI-PstI-SphI-HindIII
SELECTION
#indicator beta-galactosidase
SUMMARY M13mp18 #length 7250 #checksum 7990.
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1768 a 1538 c 1533 g 2411 t
ORIGIN
Query Match 99.9%; Score 1215.4; DB 12; Length 7250;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAAGCTTGCATGCTGCAGCTGACTAGAGATCCCGGGTACCGAGCTCGAATTC 60
Db 6290 GCCAAGCTTGCATGCTGCAGCTGACTAGAGATCCCGGGTACCGAGCTCGAATTC 6231
QY 61 GTAATCATGCTCATAGCTGTTTCCCTGTGTGAAATCTTATCCGCTCACAATTCACACAA 120
Db 6230 GTAATCATGCTCATAGCTGTTTCCCTGTGTGAAATCTTATCCGCTCACAATTCACACAA 6171
QY 121 CATAGACCGGGAACATATAAGTGTAAAGCCTGGGCTGCCTAATGAGTCAGCTAACTAC 180
Db 6170 CATAGACCGGGAACATATAAGTGTAAAGCCTGGGCTGCCTAATGAGTCAGCTAACTAC 6111
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Db 6110 ATTAATTCGTTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCTGTCAGCTGCA 6051
QY 241 TTATGATTCGCGCAACCGCGGGAGAGCGGTTTGGCTATTGGCGCGCAGGGTGGTTT 300
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Db 5990 TTCTTTTCCACAGTGAGACGGGCAACAGCTGATTCCTCCCTTACCGCCTGGCCCTGAGAGA 5931
QY 361 GTTGACCAAGCGGTCCACGCTGTTTGGCCCGCAGCGGAAATCCCTGTTGATGGTGG 420
Db 5930 GTTGACCAAGCGGTCCACGCTGTTTGGCCCGCAGCGGAAATCCCTGTTGATGGTGG 5871
QY 421 TTCCGAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCCGAGATAGGGTTGAGTGT 480
Db 5870 TTCCGAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCCGAGATAGGGTTGAGTGT 5811

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IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known: 800 n's separate segments. Unfinished: 3p213_6 Contig_ID: 01215 acc-284493 Length: 1189 bp Unfinished: 3p213_6 Contig_ID: 00286 acc-284493 Length: 25563 bp Unfinished: 3p213_6 Contig_ID: 01317 acc-284493 Length: 7251 bp Unfinished: 3p213_6 Contig_ID: 01351 acc-284493 Length: 1446 bp Unfinished: 3p213_6 Contig_ID: 01396 acc-284493 Length: 25723 bp.

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1189: contig of 1189 bp in length
 * 1190 1989: gap of 800 bp
 * 1990 27552: contig of 25563 bp in length
 * 27553 28352: gap of 800 bp
 * 28353 35603: contig of 7251 bp in length
 * 35604 36403: gap of 800 bp
 * 36404 37849: contig of 1446 bp in length
 * 37850 38649: gap of 800 bp
 * 38650 64372: contig of 25723 bp in length.

Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /clone="XXcos-LUCA6"
 /clone.lib="SCLUCA"

BASE COUNT 13403 a 16120 c 16451 g 15161 t 3237 others
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Query Match 98.7%; Score 1201.2; DB 2; Length 64372;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1214; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCCAAGCTTCATGCTGCGAGGTCGACTCTAGAGGATCCCGGTCACCGAGTCGAATTC 60
 DB 34643 GCCAAGCTTCATGCTGCGAGGTCGACTCTAGAGGATCCCGGTCACCGAGTCGAATTC 60
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 DB 34583 GTAATCATGCTCATAGCTGTTTCCCTGTGTAATTTGTTATCCGCTCACAATTCACACAA 120
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 DB 34523 CATACGAGCGGAGCATTAAGTAAAGCTTGGGTGGCTTAATGAGTGAAGTAACTAC 180
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QY 481 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGTGGACTCCAAAGCTCAAGGGCG 540
 DB 5810 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGTGGACTCCAAAGCTCAAGGGCG 5751
 QY 541 AAAAACCCTATACAGGGCGATGGCCGCTACGTGACCATCAACCAATCAAGTATTTT 600
 DB 5750 AAAAACCCTATACAGGGCGATGGCCGCTACGTGACCATCAACCAATCAAGTATTTT 5691
 QY 601 GGGTCCAGTGGCGTAAAGCAGCTAAATCGGAACCTTAAAGGAGAGCCCGCATTTAGAGC 660
 DB 5690 GGGTCCAGTGGCGTAAAGCAGCTAAATCGGAACCTTAAAGGAGAGCCCGCATTTAGAGC 5631
 QY 661 TTGACGGGAAAGCCGGGAAAGCTGGGAGAAAGGAAGGAAGGAAGGAAGGAGCGG 720
 DB 5630 TTGACGGGAAAGCCGGGAAAGCTGGGAGAAAGGAAGGAAGGAAGGAAGGAGCGG 5571
 QY 721 CGCTAGGCGCTGGCAAGTGTAGCGGTCACGCTGCGGTAAACACACACCGCGCGCT 780
 DB 5570 CGCTAGGCGCTGGCAAGTGTAGCGGTCACGCTGCGGTAAACACACACCGCGCGCT 5511
 QY 781 TAATCGCGCTACAGGGCGGTACTATGCTTTGACGAGCAGCTATACGTTGCTTT 840
 DB 5510 TAATCGCGCTACAGGGCGGTACTATGCTTTGACGAGCAGCTATACGTTGCTTT 5451
 QY 841 CCTCGTTGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAGGGATTTTAGACAGA 900
 DB 5450 CCTCGTTGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAGGGATTTTAGACAGA 5391
 QY 901 ACGGTACGCGAGAACTCTGAGAAGTGTATTAATCAGTACGAGCGGCGGCAAGAG 960
 DB 5390 ACGGTACGCGAGAACTCTGAGAAGTGTATTAATCAGTACGAGCGGCGGCAAGAG 5331
 QY 961 TCTGCTCATCAGCAATTAACGTTGTAGCAATCTCTTTGATTAGTAATAACATCAC 1020
 DB 5330 TCTGCTCATCAGCAATTAACGTTGTAGCAATCTCTTTGATTAGTAATAACATCAC 5271
 QY 1021 TTGCTGAGTAGAAGAACTCAAACTATCGGCTTGGTGAATATCCAGCAATATTAC 1080
 DB 5270 TTGCTGAGTAGAAGAACTCAAACTATCGGCTTGGTGAATATCCAGCAATATTAC 5211
 QY 1081 CGCAGCGCATTCACAGGAAAGCGCTCATGAAATACCTACATTTTTCAGCTCAATCG 1140
 DB 5210 CGCAGCGCATTCACAGGAAAGCGCTCATGAAATACCTACATTTTTCAGCTCAATCG 5151
 QY 1141 TCTCAATGGAATTTTACATTTGCGAGATTCACAGCTACAGCAGCAGTAAAGGGA 1200
 DB 5150 TCTCAATGGAATTTTACATTTGCGAGATTCACAGCTACAGCAGCAGTAAAGGGA 5091
 QY 1201 CATCTGCGCAACAGAG 1217
 DB 5090 CATCTGCGCAACAGAG 5074

RESULT 5
 HSLUCA6
 LOCUS Homo sapiens chromosome 3 clone XXcos-LUCA6, *** SEQUENCING IN
 DEFINITION
 PROGRESS *** 5 unordered pieces.
 ACCESSION 284493
 VERSION 284493.1 GI:6981854
 KEYWORDS HTG: HTGS_PHASE1.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 64372)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (12-NOV-1998) Wellcome Trust Genome Campus, Hinxton,
 JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Feb 16, 2000 this sequence version replaced gi:3334742.

Db 34223 TTTCCGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 34164
QY 481 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGCTGGACTCAAGCTCAAAAGGCG 540
Db 34163 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGCTGGACTCAAGCTCAAAAGGCG 34104
QY 541 AAAAACCTCTATCATGAGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTT 600
Db 34103 AAAAACCTCTATCATGAGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTT 34044
QY 601 GGGTCGAGGTGCCCTAAAGCACTAAATCGGAACCTTAAGGAGCGCCCGCATTTAGAGC 660
Db 34043 GGGTCGAGGTGCCCTAAAGCACTAAATCGGAACCTTAAGGAGCGCCCGCATTTAGAGC 33984
QY 661 TTGACGGGGAAGCGCGGCAAGCTGGCGGAGAAAGGAGGAAAGCAAGGAGCGGG 720
Db 33983 TTGACGGGGAAGCGCGGCAAGCTGGCGGAGAAAGGAGGAAAGCAAGGAGCGGG 33924
QY 721 CGTATGCGCGCTGCAAGTGTAGCGGTACGCTCGCGGTAAACACACACCGCGCGCT 780
Db 33923 CGTATGCGCGCTGCAAGTGTAGCGGTACGCTCGCGGTAAACACACACCGCGCGCT 33864
QY 781 TAATGCGCGCTGCAAGTGTAGCGGTACGCTCGCGGTAAACACACACCGCGCGCT 840
Db 33863 TAATGCGCGCTGCAAGTGTAGCGGTACGCTCGCGGTAAACACACACCGCGCGCT 33804
QY 841 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 900
Db 33803 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 33744
QY 901 ACGGTACGCGAGATCTTGAGAGTGTATTTTATAATCAGTGAGCGCACCGAGTAAAGAG 960
Db 33743 ACGGTACGCGAGATCTTGAGAGTGTATTTTATAATCAGTGAGCGCACCGAGTAAAGAG 33684
QY 961 TCTGTCATCAGCAAAATTAACGTTTGTAGCAATATCTTTGATTAAGTAAATCAATCAC 1020
Db 33683 TCTGTCATCAGCAAAATTAACGTTTGTAGCAATATCTTTGATTAAGTAAATCAATCAC 33624
QY 1021 TTGCTGTAGTAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGCAATATATAC 1080
Db 33623 TTGCTGTAGTAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGCAATATATAC 33564
QY 1081 CGCCAGCATTTGCAACAGGAAAGCGCTCATGGAATACCTACATTTTACGCTCAATCG 1140
Db 33563 CGCCAGCATTTGCAACAGGAAAGCGCTCATGGAATACCTACATTTTACGCTCAATCG 33504
QY 1141 TCTGAATGGAATTTTACATTTGCGAGATTACCA-GTCACAGCACGTAATAAGAGG 1199
Db 33503 TCTGAATGGAATTTTACATTTGCGAGATTACCAATGTCACAGCACGTAATAAGAGG 33444
QY 1200 ACATTTCTGGCCACAGAG 1217
Db 33443 ATATTTCTGGCCACAGAG 33426

RESULT 6
SYN13M10V/c
LOCUS SYN13M10V 7244 bp DNA circular SYN 26-JUL-1993
DEFINITION M13mp10 phage cloning vector.
ACCESSION L08819
VERSION L08819.1 GI:310747
KEYWORDS
SOURCE Synthetic construct DNA.
ORGANISM
REFERENCE 1 (bases 1 to 7244)
AUTHORS Gilbert, W.
TITLE Obtained from VecBase 3.0
JOURNAL unpublished (1991)
COMMENT These data and their annotations were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program. M13mp10 - Phage cloning vector

ENTRY M13MP10
Phage cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION VR0016
SOURCE artificial
REFERENCE
#number 1
#authors Messing J., Vieira J.
#journal Gene (1982) 19: 269-276
#comment see note added in proof
REFERENCE
#number 2
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-v-1
COMMENT Assembled from M13mp18
by W. Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):M13mp8
#parent
GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bcall12
#brother
VecBase(3):M13mp11
#offspring
VecBase(3):pUC12, VecBase(3):M13mp18, VecBase(3):M13mIC7
PARENT
Features of M13mp10 (7244 bp)
residue source
1-5868 1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6281 1- 51 M13mp10/pUC12-Polylinker
6284-6705 1303-1724 Lac-Operon
6706-7244 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp10 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6516 G T 1535 Lac
mut 6932 T C 6095 phage M13
mut 6962 T G 6125 phage M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene V.
M13mp10 contains two amber mutations in gene I and gene II.
These mutations are not presented in this sequence.
In M13mp10w the mutations have been reverted to wildtype.
FEATURE
POLYLINKER EcoRI-SacI-SmaI-BamHI-XbaI-Sall-PstI-HindIII SELECTION
#indicator beta-galactosidase
SUMMARY M13mp10 #length 7244 #checksum 6839.
Location/Qualifiers
1..7244
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1766 a 1539 c 1530 g 2409 t
ORIGIN

Query Match 97.4%; Score 1184.8; DB 12; Length 7244;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY 14 GCCTGCGAGTCTGAGAGATCCCGGCTACCGAGCTCGAATTCGTAATCATGTGCA 73
Db 6274 GCCTGCGAGTCTGAGAGATCCCGGCTACCGAGCTCGAATTCGTAATCATGTGCA 6218
QY 74 TAGCTCTTCTCTGTGAAATTTGTTATCCCGCTCACAATTCACACACATACGACCGGA 133

Db	5137	ATTACATTGGCAGATTACACAGTTCACAGCAGCAGTAAATAAAGGACATTTCTGGCCAAC	5078
Qy	1214	AGAG 1217	
Db	5077	AGAG 5074	
RESULT	7		
LOCUS	108051	9955 bp	linear
DEFINITION	Sequence 7 from Patent EP 0265293.		PAT 02-DEC-1994
ACCESSION	108051		
VERSION	108051.1	GI:589240	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 9955)		
AUTHORS	Tabor, S. and Richardson, C.C.		
TITLE	T7 DNA polymerase		
JOURNAL	Patent: EP 0265293-A2 7 27-APR-1988;		
FEATURES	Location/Qualifiers		
	1..9955		
	/organism="unknown"		
BASE COUNT	2452 a	2218 c	3039 t
ORIGIN			
	Query Match	95.7%;	Score 1165.2; DB 6; Length 9955;
	Best Local Similarity	99.7%;	Pred. No. 0;
	Matches 1167; Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	48	CGAGCTCGAATTCGTAATCATAGCTTCTCTGTGTGTAATTTGTTATCCGCTCA	107
Db	6243	CGAGCTCGAATTCGTAATCATAGCTTCTCTGTGTGTAATTTGTTATCCGCTCA	6184
Qy	108	CAATTCACACACATACGAGCGGAGCATAAAGTCTAAAGCTGGGGTGCCTAATGAG	167
Db	6183	CAATTCACACACATACGAGCGGAGCATAAAGTCTAAAGCTGGGGTGCCTAATGAG	6124
Qy	168	TGAGCTAACTCACATTAATTCGCTTGCCTCAGTCCCGCTTCCAGTCGGGAACCTGT	227
Db	6123	TGAGCTAACTCACATTAATTCGCTTGCCTCAGTCCCGCTTCCAGTCGGGAACCTGT	6064
Qy	228	CGTGGCAGCTGCATTAATGAAATCGCCCAACCGCGGAGAGCGGTTTGGCTATTGGGC	287
Db	6063	CGTGGCAGCTGCATTAATGAAATCGCCCAACCGCGGAGAGCGGTTTGGCTATTGGGC	6004
Qy	288	CCCAGGGTGGTTTCTTTTCCAGTGCAGACGGGCAACAGCTGATTCGCCCTTCACCGCC	347
Db	6003	CCCAGGGTGGTTTCTTTTCCAGTGCAGACGGGCAACAGCTGATTCGCCCTTCACCGCC	5944
Qy	348	TGGCCCTGAGAGAGTTGAGCAAGCGGTCACGCTGGTTTGGCCAGCAGCGGAAATCC	407
Db	5943	TGGCCCTGAGAGAGTTGAGCAAGCGGTCACGCTGGTTTGGCCAGCAGCGGAAATCC	5884
Qy	408	TGTTTGTAGTGGTTCGCAAAATCGCAAAATCCCTTATATAATCAAAAGAAATAGCCGAGA	467
Db	5883	TGTTTGTAGTGGTTCGCAAAATCGCAAAATCCCTTATATAATCAAAAGAAATAGCCGAGA	5824
Qy	468	TAGGTTGAGTGTGTTCAGTTTGGAAACAGAGTCCACTATTAAGAAGCTGGACTCCA	527
Db	5823	TAGGTTGAGTGTGTTCAGTTTGGAAACAGAGTCCACTATTAAGAAGCTGGACTCCA	5764
Qy	528	AGCTCAAGGGCGGAAACCGCTCTATCAGGGGATGGCCACTTACCTGTAACCATCACCCA	587
Db	5763	AGCTCAAGGGCGGAAACCGCTCTATCAGGGGATGGCCACTTACCTGTAACCATCACCCA	5704
Qy	588	AATCAAGTTTGTGGGGTGGAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGCC	647
Db	5703	AATCAAGTTTGTGGGGTGGAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGCC	5644
Qy	648	CCCGATTAGAGCTTGACGGGGAAAGCCGCGGAAAGCTGGCGGAGAAAGGAAGAAAG	707

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Db 5643 CCCGATTAGAGCTTGACGGGAAAGCCGCGAACGTCGCGAGAAAGGGAAGAAAG 5584
Qy 708 CGAAGAGAGCGGCGCTAGGCGCTGGCAAGCTGTAGCGGTACGCTGCGGTAAACACCA 767
Db 5583 CGAAGAGAGCGGCGCTAGGCGCTGGCAAGCTGTAGCGGTACGCTGCGGTAAACACCA 5524
Qy 768 CACCGCGCGGCTTAAATGCGCGCTACAGGCGCGTACTATGTTGCTTTCACGAGCAG 827
Db 5523 CACCGCGCGGCTTAAATGCGCGCTACAGGCGCGTACTATGTTGCTTTCACGAGCAG 5464
Qy 828 TATAACCTGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTTAAAGG 887
Db 5463 TATAACCTGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTTAAAGG 5404
Qy 888 ATTTTAGACAGGAGCGTACGCGAGATCTTGAGAACTGTTTATATATACAGTACGAGCCA 947
Db 5403 ATTTTAGACAGGAGCGTACGCGAGATCTTGAGAACTGTTTATATACAGTACGAGCCA 5344
Qy 948 CCAGTAAAGAGCTGTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTTAAAGG 1007
Db 5343 CCAGTAAAGAGCTGTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTTAAAGG 5284
Qy 1008 GTAATACATCACTTCCCTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCC 1067
Db 5283 GTAATACATCACTTCCCTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCC 5224
Qy 1068 AGAACAATATTACCGCAGCCATTTGCAACAGGAAACGCTCATGGAATACCTACATTT 1127
Db 5223 AGAACAATATTACCGCAGCCATTTGCAACAGGAAACGCTCATGGAATACCTACATTT 1127
Qy 1128 TGACGCTCAATGCTGCTGAAATGATTATTTACATTTGGCAGATTCACGAGTACACGACCA 1187
Db 5163 TGACGCTCAATGCTGCTGAAATGATTATTTACATTTGGCAGATTCACGAGTACACGACCA 5104
Qy 1188 GTAATAAAGGACATCTGCGCAACAGAG 1217
Db 5103 GTAATAAAGGACATCTGCGCAACAGAG 5074

RESULT 8
SYNM13MP2V/c SYNM13MP2V 7196 bp DNA circular SYN 26-JUL-1993
LOCUS M13mp2 phage cloning vector.
DEFINITION L08818
ACCESSION L08818
VERSION L08818.1 GI:310751
KEYWORDS Synthetic construct DNA.
SOURCE artificial sequence.
ORGANISM Gilbert,W.
REFERENCE 1 (bases 1 to 7196)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mp2
- Phage cloning vector
ENTRY M13MP2 #TYPE DNA CIRCULAR TITLE M13mp2 -
Phage cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION V00012
SOURCE artificial
REFERENCE
#number 1
#authors Gronenborn B., Messing J.
#journal Nature (1978) 272: 375-377
COMMENT
Assembled from M13mp7
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE

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#parent
VecBase(3):M13mp1
#parent
GenBank(50):M13, GenBank(50):EcoLac, GenBank(50):M13EcoLac
#offspring
VecBase(3):M13mp7
PARENT
Features of M13mp2 (7196 bp)
residue source
1-5868 1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6236 1-6 EcoRI site
6237-6657 1304-1724 Lac-Operon
6658-7196 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp2 source
cfl 5977 G A 1044 Lac
cfl 6468 G T 1535 Lac
mut 6914 T G 6125 phage M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene V.
FEATURE
POLYLINKER none
SELECTION
#indicator beta-galactosidase
SUMMARY M13mp2 #length 7196 #checksum 3751.
Location/Qualifiers
1..7196
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1757 a 1524 c 1516 g 2399 t
ORIGIN
Query Match 95.4%; Score 1161.4; DB 12; Length 7196;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 55 GAATTCGTAATCAATGTCATAGCTGTTCTGTGTGTAATTTGTTATCCGCTCACAATTC 114
Db 6236 GAATTCGTAATCAATGTCATAGCTGTTCTGTGTGTAATTTGTTATCCGCTCACAATTC 6177
Qy 115 ACACAACATACGAGCGCGGAGCAATAAGTGTAAAGCTTGGGTGCTTAAATGAGTGAGCTA 174
Db 6176 ACACAACATACGAGCGCGGAGCAATAAGTGTAAAGCTTGGGTGCTTAAATGAGTGAGCTA 6117
Qy 175 ACTCACATTAATGCTTCCGCTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 234
Db 6116 ACTCACATTAATGCTTCCGCTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 6057
Qy 235 GCTGCATTAATGAATCGGCCAACGCGGAGAGCGGTTTCCGATTTGGGCGCCAGG 294
Db 6056 GCTGCATTAATGAATCGGCCAACGCGGAGAGCGGTTTCCGATTTGGGCGCCAGG 5997
Qy 295 TGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCTTTCACGCTGCGCCCT 354
Db 5996 TGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCTTTCACGCTGCGCCCT 5937
Qy 355 CAGAGAGTTGCAGCAAGCGTCCAGCTGTTGCCCCAGCAGCGGAAATCCTGTTGA 414
Db 5936 CAGAGAGTTGCAGCAAGCGTCCAGCTGTTGCCCCAGCAGCGGAAATCCTGTTGA 5877
Qy 415 TGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTT 474
Db 5876 TGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTT 5817
Qy 475 GAGTGGTTTCCAGCTTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCCAAAGTCAA 534
Db 5816 GAGTGGTTTCCAGCTTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCCAAAGTCAA 5757
Qy 535 AGGCGGAAAAACCGTCTATCAGGCGGATGCGCCACTACGTTGAACCATCACCAATCAAG 594

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Db 5756 AGGGGAAAAACCGTCTATCAGGCGATGGCCCACTACGTGAACCAATACCCCAATCAAG 5697

Qy 595 TTTTGGGCTCCAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGGCCCGCGATT 654

Db 5696 TTTTGGGCTCCAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGGCCCGCGATT 5637

Qy 655 TAGAGCTTGACGGGAAAGCCGGGAAAGCGTGGGAGNAAGGAAGGAAGCAAGG 714

Db 5636 TAGAGCTTGACGGGAAAGCCGGGAAAGCGTGGGAGNAAGGAAGGAAGCAAGG 5577

Qy 715 AGCGGGGCTAGGCGCTGCAAGTGTAGCGGTACCGCTGCGGTAAACCAACACCCCGC 774

Db 5576 AGCGGGGCTAGGCGCTGCAAGTGTAGCGGTACCGCTGCGGTAAACCAACACCCCGC 5517

Qy 775 CGCGCTTAATCGCGCTACAGGCGGTACTATGTTGCTTTCACGAGCACGTATACG 834

Db 5516 CGCGCTTAATCGCGCTACAGGCGGTACTATGTTGCTTTCACGAGCACGTATACG 5457

Qy 835 TGCTTTCCTCGTGGAAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAAGGGATTAG 894

Db 5456 TGCTTTCCTCGTGGAAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAAGGGATTAG 5397

Qy 895 ACAGGAACGGTACGCGAAGCTTGAAGTGTATTAATCACTAGTGAAGCCAGCAGTA 954

Db 5396 ACAGGAACGGTACGCGAAGCTTGAAGTGTATTAATCACTAGTGAAGCCAGCAGTA 5337

Qy 955 AAAGAGTCTGTCATCACCAATTAACCGTTGTAGCAATACCTCTTGTATTAGTAATAA 1014

Db 5336 AAAGAGTCTGTCATCACCAATTAACCGTTGTAGCAATACCTCTTGTATTAGTAATAA 5277

Qy 1015 CATCACTTGCTGAGTAGAAGAACTCAAACTATCGGCCCTGCTGTAATATCCAGAACAA 1074

Db 5276 CATCACTTGCTGAGTAGAAGAACTCAAACTATCGGCCCTGCTGTAATATCCAGAACAA 5217

Qy 1075 TATTACGCGCAGTTCGCAAGCAAGAAACGCTCATGGAATACCTACATTTGACGCT 1134

Db 5216 TATTACGCGCAGTTCGCAAGCAAGAAACGCTCATGGAATACCTACATTTGACGCT 5157

Qy 1135 CAATCGTCTGAATGGATTATTTACATTTGGCAGATTCCAGTCCACGACCACTAATAA 1194

Db 5156 CAATCGTCTGAATGGATTATTTACATTTGGCAGATTCCAGTCCACGACCACTAATAA 5097

Qy 1195 AAGGACATCTTGCCCAACAGAG 1217

Db 5096 AAGGACATCTTGCCCAACAGAG 5074

RESULT 9

SYNMI3MP8V/c SYNMI3MP8V 7229 bp DNA circular SYN 08-FEB-2002

LOCUS SYNMI3MP8V M13mp8 phage cloning vector.

DEFINITION M13mp8 phage cloning vector.

ACCESSION M77826 M28279

VERSION M77826.1 GI:208804

KEYWORDS Synthetic construct DNA.

SOURCE Synthetic construct

ORGANISM artificial sequence.

REFERENCE 1 (sites)

AUTHORS Messing, J. and Vieira, J.

TITLE A new pair of M13 vectors for selecting either DNA strand of double-digest restriction fragments

JOURNAL Gene 19 (3), 269-276 (1982)

MEDLINE 83106471

REFERENCE 2 (bases 1 to 7229)

AUTHORS Gilbert, W.

TITLE Obtained from VecBase 3.0

JOURNAL Unpublished (1991)

COMMENT On Feb 8, 2002 this sequence version replaced gi:341882. These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program. M13mp8 - Phage cloning vector

ENTRY M13MP8

Phage cloning vector

DATE 10-OCT-1985

#sequence 02-APR-1986

ACCESSION VB0014

SOURCE artificial

REFERENCE

#number 1

#authors Messing J., Vieira J.

#journal Gene (1982) 19: 269-276

#comment see also 'note added in proof'

REFERENCE

#number 2

#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.

#book Cloning Vectors, Elsevier 1985 and supplements

#comment vector I-A-v-1

COMMENT

Assembled from M13mp18

by William Gilbert, Whitaker College, MIT and

by F. Pfeiffer, MPI, Martinsried

KEYWORDS

CROSSREFERENCE

#parent

VecBase(3):M13mp7

#parent

GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bga18

#brother

VecBase(3):M13mp9

#offspring

VecBase(3):pUC8, VecBase(3):M13mp10

PARENT

Features of M13mp8 (7229 bp)

residue source

1-5868 1-5868 phage M13

5869-6230 936-1297 Lac-Operon

6231-6266 1-36 M13mp8/pUC8-Polylinker

6269-6690 1303-1724 Lac-Operon

6691-7229 5869-6407 phage M13

Conflict (cfl) and Mutations (mut):

M13mp8 source

mut 3 T C 3 phage M13

mut 2220 A G 2220 phage M13

cfl 5977 G A 1044 Lac

cfl 6501 G T 1535 Lac

mut 6917 T C 6095 phage M13

mut 6947 T G 6125 phage M13

Position 898 is TT in Messing's sequence, but TTT in M13

wildtype.

It was changed to TTT to restore the reading frame of gene V.

M13mp8 contains two amber mutations in gene I and gene II.

These mutations are not presented in this sequence. FEATURE

POLYLINKER ECORI-SmaI-BamHI-SalI-PstI-HindIII

SELECTION

#indicator beta-galactosidase

SUMMARY M13mp8 #length 7229 #checksum 7311.

Location/Qualifiers

1. 7229

/organism="synthetic construct"

/db_xref="taxon:32650"

BASE COUNT 1763 a 1534 c 1526 g 2406 t

ORIGIN

Query Match 95.4%; Score 1161.4; DB 12; Length 7229;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 55 GAATTCGTAATCATGTCATAGCTGTTTCCTGCTGTAATTTTCGCTCACAAATTC 114

Db 6236 GAATTCGTAATCATGTCATAGCTGTTTCCTGCTGTAATTTTCGCTCACAAATTC 6177

Qy 115 ACACACATACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 174

Db 6176 ACACACATACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6117

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QY 175 ACTCACATTAATGCGTTCGCTCACTGCCGCTTTCCAGTGGGAACCTGCTGCCA 234
Db 6116 ACTCACATTAATGCGTTCGCTCACTGCCGCTTTCCAGTGGGAACCTGCTGCCA 6057
QY 235 GCTGCAATTAATGCGTTCGCTCACTGCCGCTTTCCAGTGGGAACCTGCTGCCA 6057
Db 6056 GCTGCAATTAATGCGTTCGCTCACTGCCGCTTTCCAGTGGGAACCTGCTGCCA 294
QY 295 TGGTTTTTCTTTCACCACTGAGACGGCAACAGCTGATTGGCCTTACCGCTGCCCT 354
Db 5996 TGGTTTTTCTTTCACCACTGAGACGGCAACAGCTGATTGGCCTTACCGCTGCCCT 354
QY 355 GAGAGAGTTGACGAGGCGTCCAGCTGCTTTGCCAGCAGGCGAAATCCTGTTCA 414
Db 5936 GAGAGAGTTGACGAGGCGTCCAGCTGCTTTGCCAGCAGGCGAAATCCTGTTCA 5877
QY 415 TGGTGGTTCGGAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGTAGGTT 474
Db 5876 TGGTGGTTCGGAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGTAGGTT 5817
QY 475 GAGTGTGTTGTCAGTTGGAACAGAGTCCACTATTAAAGAACGTGGACTCAACGTCAA 534
Db 5816 GAGTGTGTTGTCAGTTGGAACAGAGTCCACTATTAAAGAACGTGGACTCAACGTCAA 5757
QY 535 AGGCGGAAAAACCGTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCAATCAAG 594
Db 5756 AGGCGGAAAAACCGTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCAATCAAG 5697
QY 595 TTTTTCGGGTCGAGGTGCGTAAAGCACTAAATCGGAACCTAAAGGAGCCCGGATT 654
Db 5696 TTTTTCGGGTCGAGGTGCGTAAAGCACTAAATCGGAACCTAAAGGAGCCCGGATT 5637
QY 655 TAGAGCTTGACGGGAAAGCGCGAACGTGGCGAGAAAGGAGGAGAAAGCAAGG 714
Db 5636 TAGAGCTTGACGGGAAAGCGCGAACGTGGCGAGAAAGGAGGAGAAAGCAAGG 5577
QY 715 ACGGCGGCTAGGCGGCTGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCGC 774
Db 5576 ACGGCGGCTAGGCGGCTGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCGC 5517
QY 775 CCGGCTTAATGCGCGCTACAGGCGCGTACTATGCTTTCAGGACGACGTATAACG 834
Db 5516 CCGGCTTAATGCGCGCTACAGGCGCGTACTATGCTTTCAGGACGACGTATAACG 894
QY 835 TGTCTTCTCTGTTGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGATTTAG 894
Db 5456 TGTCTTCTCTGTTGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGATTTAG 5397
QY 895 ACAGGACGGTACGCCAGATTTGAGAGTGTGTTTATATACGTGAGGCCACCGAGTA 954
Db 5396 ACAGGACGGTACGCCAGATTTGAGAGTGTGTTTATATACGTGAGGCCACCGAGTA 5337
QY 955 AAAGAGTCTGCCATCAGCAATTAACCGTTGAGCAATCTCTTTGATTAGTAATAA 1014
Db 5336 AAAGAGTCTGCCATCAGCAATTAACCGTTGAGCAATCTCTTTGATTAGTAATAA 5277
QY 1015 CATCACTTGGCTGAGTGAAGAACTCAAACTATCGGCTTCTGTTAATATCCAGACAA 1074
Db 5276 CATCACTTGGCTGAGTGAAGAACTCAAACTATCGGCTTCTGTTAATATCCAGACAA 5217
QY 1075 TATTACCGCCAGCATTTGCAACAGGAAACGCTCATGGAATACCTACATTTGAGCT 1134
Db 5216 TATTACCGCCAGCATTTGCAACAGGAAACGCTCATGGAATACCTACATTTGAGCT 5157
QY 1135 CAATCGTCTGAATGGAATTTATATGTCAGATTCCACAGTCCACAGCAGTATAA 1194
Db 5156 CAATCGTCTGAATGGAATTTATATGTCAGATTCCACAGTCCACAGCAGTATAA 5097
QY 1195 AAGGACATTTCTGGCCCAACAGAG 1217
Db 5096 AAGGACATTTCTGGCCCAACAGAG 5074
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RESULT 10
SYNPU8CPL/C SYNPU8CPL
LOCUS M13mp8/pUC8 7229 bp ss-DNA linear SYN 07-MAR-2000
DEFINITION M13mp8/pUC8 cloning vector.
ACCESSION M77689
VERSION M77689.1 GI:310826
KEYWORDS beta-galactosidase; lac gene.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Vieira, J. and Messing, J.
TITLE The pUC plasmids, an M13mp7-derived system for insertion
JOURNAL mutagenesis and sequencing with synthetic universal primers
MEDLINE Gene 19, 259-268 (1982)
REFERENCE 2 (bases 1 to 7229)
AUTHORS Messing, J. and Vieira, J.
TITLE A new pair of M13 vectors for selecting either DNA strand of
JOURNAL double-digest restriction fragments
MEDLINE Gene 19, 269-276 (1982)
FEATURES
source Location/Qualifiers
1..7229
/organism="synthetic construct"
/db_xref="taxon:32630"
/focus
1..5868
/organism="Coliphage M13"
/db_xref="taxon:10870"
5869..6230
/organism="Escherichia coli"
/feature="Lac-Operon"
/db_xref="taxon:562"
6231..6266
/organism="synthetic construct"
/feature="M13mp8/pUC8-Polylinker"
/db_xref="taxon:32630"
6269..6690
/organism="Escherichia coli"
/db_xref="taxon:562"
6691..7229
/organism="Coliphage M13"
/db_xref="taxon:10870"
BASE COUNT 1763 a 1534 c 1526 g 2406 t
ORIGIN

Query Match 95.4%; Score 1161.4; DB 12; Length 7229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 GAATTCGTAATCATGTCATAGCTGTTCTCTGTGTAAGATTTGTAATCCGCTCAAAATTC 114
Db 6236 GAATTCGTAATCATGTCATAGCTGTTCTCTGTGTAAGATTTGTAATCCGCTCAAAATTC 6177
QY 115 ACACACATACAGCGCGGAGCAATAAGTGTAAAGCTGGGTCGCTTAATGAGTGAGCTA 174
Db 6176 ACACACATACAGCGCGGAGCAATAAGTGTAAAGCTGGGTCGCTTAATGAGTGAGCTA 6117
QY 175 ACTCATTAATTAATGCTTGCCTCACTGCCGCTTTCAGTGGGAGAGCGGTTTCCCTATTGGCGCCAGG 234
Db 6116 ACTCATTAATTAATGCTTGCCTCACTGCCGCTTTCAGTGGGAGAGCGGTTTCCCTATTGGCGCCAGG 6057
QY 235 GCTGCATTAATGAATCGGCCAACCGCGGAGAGCGGTTTGCCTATTGGCGCCAGG 294
Db 6056 GCTGCATTAATGAATCGGCCAACCGCGGAGAGCGGTTTGCCTATTGGCGCCAGG 5997
QY 295 TGGTTTTTCTTTCACCACTGAGACGGCAACAGCTGATTGGCCTTACCGCTGCCCT 354
Db 5996 TGGTTTTTCTTTCACCACTGAGACGGCAACAGCTGATTGGCCTTACCGCTGCCCT 5937
QY 355 GAGAGAGTTGACGAGGCGTCCAGCTGCTTTGCCAGCAGGCGAAATCCTGTTCA 414
```


Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mic7
- Phase cloning vector
ENTRY M13mic7
#TYPE DNA CIRCULAR TITLE M13mic7 -
Phase cloning vector
DATE 25-FEB-1987
ACCESSION V0099
SOURCE artificial
REFERENCE
#number 1
#authors Marsh J.L., Erle M., Wykes E.J.
#journal Gene (1984) 32: 481-485
#title
The p1C plasmid and phage vectors with versatile cloning
sites for recombinant selection by insertional inactivation
COMMENT
Assembled from M13mp10 and GenBank:p1C7 by F. Pfeiffer
For construction of p1C7, a synthetic oligonucleotide has been
used to replace the pUC7 polylinker and thus to construct a
new cloning vector with a different polylinker. Replacement of
the polylinker of M13mp10 with this new polylinker resulted in
M13mic7.
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3): M13mp10, GenBank(50): p1C7
PARENT
Features of M13mic7 (7232 bp)
residue source
1-6236 1-6236 M13mp10
6231-6269 1-39 polylinker of p1C7
6264-7232 6276-7244 M13mp10
Conflict (cfl) and Mutations (mut): none
FEATURE
POLYLINKER EcoRI-ClaI-EcoRV-XbaI-BglII-XhoI-SacI-NruI-HindIII
SELECTION
#indicator beta-galactosidase
SUMMARY M13mic7 #length 7232 #checksum 2693.
Location/Qualifiers
1. 7232
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1767 a 1531 c 1524 g 2410 t
ORIGIN
Query Match 95.4%; Score 1161.4; DB 12; Length 7232;
Rest Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 1; Indels 0; Gaps 0;
QY 55 GAATTCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCGCTCACAATTC 114
DB 6236 GAATTCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCGCTCACAATTC 6177
QY 115 ACACAACATACGACCGGAGCAATAAAGCTGTAAGCTGGGCTGCTTAATGAGTGAGCTA 174
DB 6176 ACACAACATACGACCGGAGCAATAAAGCTGTAAGCTGGGCTGCTTAATGAGTGAGCTA 6117
QY 175 ACTCATTAAATTTGCTTGCCTCCTCCTGCTGCTTTCAGTTCGGAACCTGCTGCTCA 234
DB 6116 ACTCATTAAATTTGCTTGCCTCCTCCTGCTGCTTTCAGTTCGGAACCTGCTGCTCA 6057
QY 235 GCTGATTAAATGCTGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCGCAGG 294
DB 6056 GCTGATTAAATGCTGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCGCAGG 5997
QY 295 TGGTTTCTCTTTTACACAGTGAAGCGGCAACAGCTGATTTGCTTCCCTTCCGCTTCC 354
DB 5996 TGGTTTCTCTTTTACACAGTGAAGCGGCAACAGCTGATTTGCTTCCCTTCCGCTTCC 5937
QY 355 GAGAGAGTTGACAGAGCGGTCCACCTGGTTTGGCCCGACGAGCAATATCTGTTTGA 414

JOURNAL
COMMENT
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mic7
- Phase cloning vector
ENTRY M13mic7
#TYPE DNA CIRCULAR TITLE M13mic7 -
Phase cloning vector
DATE 25-FEB-1987
ACCESSION V0099
SOURCE artificial
REFERENCE
#number 1
#authors Marsh J.L., Erle M., Wykes E.J.
#journal Gene (1984) 32: 481-485
#title
The p1C plasmid and phage vectors with versatile cloning
sites for recombinant selection by insertional inactivation
COMMENT
Assembled from M13mp10 and GenBank:p1C7 by F. Pfeiffer
For construction of p1C7, a synthetic oligonucleotide has been
used to replace the pUC7 polylinker and thus to construct a
new cloning vector with a different polylinker. Replacement of
the polylinker of M13mp10 with this new polylinker resulted in
M13mic7.
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3): M13mp10, GenBank(50): p1C7
PARENT
Features of M13mic7 (7232 bp)
residue source
1-6236 1-6236 M13mp10
6231-6269 1-39 polylinker of p1C7
6264-7232 6276-7244 M13mp10
Conflict (cfl) and Mutations (mut): none
FEATURE
POLYLINKER EcoRI-ClaI-EcoRV-XbaI-BglII-XhoI-SacI-NruI-HindIII
SELECTION
#indicator beta-galactosidase
SUMMARY M13mic7 #length 7232 #checksum 2693.
Location/Qualifiers
1. 7232
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1767 a 1531 c 1524 g 2410 t
ORIGIN
Query Match 95.4%; Score 1161.4; DB 12; Length 7232;
Rest Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 1; Indels 0; Gaps 0;
QY 55 GAATTCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCGCTCACAATTC 114
DB 6236 GAATTCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCGCTCACAATTC 6177
QY 115 ACACAACATACGACCGGAGCAATAAAGCTGTAAGCTGGGCTGCTTAATGAGTGAGCTA 174
DB 6176 ACACAACATACGACCGGAGCAATAAAGCTGTAAGCTGGGCTGCTTAATGAGTGAGCTA 6117
QY 175 ACTCATTAAATTTGCTTGCCTCCTCCTGCTGCTTTCAGTTCGGAACCTGCTGCTCA 234
DB 6116 ACTCATTAAATTTGCTTGCCTCCTCCTGCTGCTTTCAGTTCGGAACCTGCTGCTCA 6057
QY 235 GCTGATTAAATGCTGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCGCAGG 294
DB 6056 GCTGATTAAATGCTGCAACCGCGGGAGAGCGGTTTTCGCTATTTGGCGCGCAGG 5997
QY 295 TGGTTTCTCTTTTACACAGTGAAGCGGCAACAGCTGATTTGCTTCCCTTCCGCTTCC 354
DB 5996 TGGTTTCTCTTTTACACAGTGAAGCGGCAACAGCTGATTTGCTTCCCTTCCGCTTCC 5937
QY 355 GAGAGAGTTGACAGAGCGGTCCACCTGGTTTGGCCCGACGAGCAATATCTGTTTGA 414

LOCUS
SYNICTV/c 7232 bp DNA circular SYN 26-JUL-1993
DEFINITION
M13mic7 phase cloning vector.
ACCESSION
L08836
VERSION
L08836.1 GI:310754
KEYWORDS
Synthetic construct DNA.
SOURCE
synthetic construct
ORGANISM
artificial sequence.
REFERENCE
1 (bases 1 to 7232)
AUTHORS
Gilbert.W.
TITLE
Obtained from VecBase 3.0

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Db 5936 GAGAGAGTTGCACGAAGCGTCCACGCTGTTGGCCCCAGCGGAAATCCTGTTGA 5877
QY 415 TGCTGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTT 474
Db 5876 TGGTGTTCGGAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTT 5817
QY 475 GAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAAGCTGGACTCCACAGTCAA 534
Db 5816 GAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAAGCTGGACTCCACAGTCAA 5757
QY 535 AGGCGGAAAAACCGTCTATCAGGCGGATGCGCCACTAGTGAACATCACCCAAATCAAG 594
Db 5756 AGGCGGAAAAACCGTCTATCAGGCGGATGCGCCACTAGTGAACATCACCCAAATCAAG 5697
QY 595 TTTTGTGGGTCGAGGTGCGCTAAAGCACTAAATCGGAACCTAAAGGAGCCCGCCGATT 654
Db 5696 TTTTGTGGGTCGAGGTGCGCTAAAGCACTAAATCGGAACCTAAAGGAGCCCGCCGATT 5637
QY 655 TAGAGCTTTAGCGGGAAGCGCGAACGTCGCGAGAAAGGAGGAAAGCGAAAGG 714
Db 5636 TAGAGCTTTAGCGGGAAGCGCGAACGTCGCGAGAAAGGAGGAAAGCGAAAGG 5577
QY 715 AGCGGCGCTAGGCGGCTGCGAAGTGTAGCGGTACGCTGCGGTAAACACACACCGCG 774
Db 5576 AGCGGCGCTAGGCGGCTGCGAAGTGTAGCGGTACGCTGCGGTAAACACACACCGCG 5517
QY 775 CGCGCTTAATGCGCGCTACAGGCGGCTACTATGTTGCTTTGACGACGATATAACG 834
Db 5516 CGCGCTTAATGCGCGCTACAGGCGGCTACTATGTTGCTTTGACGACGATATAACG 894
QY 835 TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGATTTAG 5397
Db 5456 TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGATTTAG 5397
QY 895 ACAGGAACGGTAGCGCAGAACTTCAGAGTCTTTTATATCACTAGTGAGCGCACGAGTA 954
Db 5396 ACAGGAACGGTAGCGCAGAACTTCAGAGTCTTTTATATCACTAGTGAGCGCACGAGTA 5337
QY 955 AAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAATA 1014
Db 5336 AAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAATA 5277
QY 1015 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGATATATCCAGAACAA 1074
Db 5276 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGATATATCCAGAACAA 5217
QY 1075 TATTACCGCCAGCCATTGCCACAGGAAACCGCTCATGGAATACCTTACATTTTGAGCGT 1134
Db 5216 TATTACCGCCAGCCATTGCCACAGGAAACCGCTCATGGAATACCTTACATTTTGAGCGT 5157
QY 1135 CAATCGTCTGAAATGGATTATTTACATTGGCAGATTCCACGATCACACGACGATATAA 1194
Db 5156 CAATCGTCTGAAATGGATTATTTACATTGGCAGATTCCACGATCACACGACGATATAA 5097
QY 1195 AAGGGACATTCTGCGCAACAGAG 1217
Db 5096 AAGGGACATTCTGCGCAACAGAG 5074

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RESULT 12
LOCUS SYN13MP7V/c 7238 bp DNA circular SYN 27-APR-1993
DEFINITION M13mp7 phage cloning vector.
ACCESSION M77569 M25456
VERSION M77569.1 GI:208803
KEYWORDS
SOURCE Synthetic construct DNA.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Messing, J., Crea R. and Seeburg, P.H.
TITLE A system for shotgun DNA sequencing
JOURNAL Nucleic Acids Res. 9, 309-321 (1981)

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MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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81150468
2 (sites)
Vieira, J. and Messing, J.
The pUC plasmids, an M13mp7-derived system for insertion
mutagenesis and sequencing with synthetic universal primers
Gene 19, 259-268 (1984)
83106470
3 (bases 1 to 7238)
Gilbert, W.
Obtained from VecBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mp7
ENTRY M13MP7
Phage cloning vector
#TYPE DNA CIRCULAR TITLE M13mp7 -
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION VB0013
SOURCE artificial
REFERENCE
#number 1
#authors Messing J., Crea R., Seeburg P.H.
#journal Nucleic Acids Res. (1981) 9: 309-321
#title A system for shotgun DNA sequencing
REFERENCE
#number 2
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-V-1
COMMENT
Assembled from M13mp8
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):M13mp2
#parent
GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bgal7
#offspring
VecBase(3):pUC7, VecBase(3):M13mp8, VecBase(3):M13mp9
VecBase(3):M13tg130, VecBase(3):M13tg131
PARENT
Features of M13mp7 (7238 bp)
residue source
1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6278 1-48 M13mp7/pUC7-Polylinker
6279-6699 1304-1724 Lac-Operon
6700-7238 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp7 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6510 G T 1535 Lac
mut 6926 T C 6095 phage M13
mut 6956 T G 6125 phage M13
#comment
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene V.
#comment
M13mp7 contains two amber mutations in M13 gene I and gene II.
These mutations are not presented in this sequence. FEATURE
POLYLINKER EcoRI-BamHI-SalI-PstI-SalI-BamHI-EcoRI SELECTION
#indicator beta-galactosidase
SUMMARY M13mp7 #length 7238 #checksum 8176.
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

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FEATURES
source

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Best Local Similarity	99.9%	Pred. No. 0			
Matches 1162	Conservative	0	Mismatches	1	Indels 0
					Gaps 0
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Db	6236	GAATTGCTAATCATGGTCTAGCTGTTTCCCTGTGTCAAAATGTTATCCCGCTCACAATTC	6177		
QY	115	ACACAACATACAGCGCGGAGGATAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTA	174		
Db	6176	ACACAACATACAGCGCGGAGGATAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTA	6117		
QY	175	ACTCAGATTAATGCTGTTGGCTACCTCCCGCTTCCAGTCGGGAAACCTGCTGTC	234		
Db	6116	ACTCAGATTAATGCTGTTGGCTACCTCCCGCTTCCAGTCGGGAAACCTGCTGTC	6057		
QY	235	GCTGCATTAATGAATCGGCAACCGCGGAGAGGCGGTTTGGCTATTGGGCGCCAGG	294		
Db	6056	GCTGCATTAATGAATCGGCAACCGCGGAGAGGCGGTTTGGCTATTGGGCGCCAGG	5997		
QY	295	TGCTTTTCTTTTACACAGTGAGAGCGGCAACAGCTGATTGCCCTTACCGCTGCGCT	354		
Db	5996	TGCTTTTCTTTTACACAGTGAGAGCGGCAACAGCTGATTGCCCTTACCGCTGCGCT	5937		
QY	355	GAGAGAGTTCAGCAAGCGTCCACAGCTGTTTCCCGCAGGCGGAAATCCCTGTTGA	414		
Db	5936	GAGAGAGTTCAGCAAGCGTCCACAGCTGTTTCCCGCAGGCGGAAATCCCTGTTGA	5877		
QY	415	TGCTGTTTCCGAAATCGGCAAAATCCCTTATAATCAAAAGATAGCCGAGATAGGTT	474		
Db	5876	TGCTGTTTCCGAAATCGGCAAAATCCCTTATAATCAAAAGATAGCCGAGATAGGTT	5817		
QY	475	GAGTGTGTTCCAGTTCGCAACAGAGTCCACTATTAAAGACGTGGACTCCACGTC	534		
Db	5816	GAGTGTGTTCCAGTTCGCAACAGAGTCCACTATTAAAGACGTGGACTCCACGTC	5757		
QY	535	AGGCGGAAACACCTCTATACAGGCGATGGCCCTACTAGCTGAACCATCACCCAAATCAAG	594		
Db	5756	AGGCGGAAACACCTCTATACAGGCGATGGCCCTACTAGCTGAACCATCACCCAAATCAAG	5697		
QY	595	TTTTTGGGTCGAGGTCGCTTAAGCACTAAATCGGACCTTAAGGAGGCGCCCGATT	654		
Db	5696	TTTTTGGGTCGAGGTCGCTTAAGCACTAAATCGGACCTTAAGGAGGCGCCCGATT	5637		
QY	655	TAGAGCTGACGGGAAACCGCGGCAACGTCGGGAGAAAGGAGGAGGAAAGCGAAAGG	714		
Db	5636	TAGAGCTGACGGGAAACCGCGGCAACGTCGGGAGAAAGGAGGAGGAAAGCGAAAGG	5577		
QY	715	AGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACACACACCCCG	774		
Db	5576	AGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACACACACCCCG	5517		
QY	775	CCGCTTAAATGCGCGCTACAGGCGCGTACTATGTTCTTTGACGAGCACGTATAAG	834		
Db	5516	CCGCTTAAATGCGCGCTACAGGCGCGTACTATGTTCTTTGACGAGCACGTATAAG	5457		
QY	835	TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGGCGGATTAAGGATTTAG	894		
Db	5456	TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGGCGGATTAAGGATTTAG	5397		
QY	895	ACAGGAACCGGTACGCGAGAACTTTGAGAGTGTGTTTATATCACTGAGGCGCCAGTA	954		
Db	5396	ACAGGAACCGGTACGCGAGAACTTTGAGAGTGTGTTTATATCACTGAGGCGCCAGTA	5337		
QY	955	AAAGAGTCTGCTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTATAA	1014		
Db	5336	AAAGAGTCTGCTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTATAA	5277		
QY	1015	CATCACTTGCTGAGTAGAGAACTCAAACTATCGGCGCTTGGTGTAAATATCCAGAACAA	1074		

Db	5276	CATCACTTGCTGAGTAGAAGAACTCAAACTATCGGCTTGCTGTAATATCCAGAACAA	5217		
QY	1075	TATTACCGCAGCCATTGCAACAGAAACGCTCATGGAATACCTACATTTTGACGCT	1134		
Db	5216	TATTACCGCAGCCATTGCAACAGAAACGCTCATGGAATACCTACATTTTGACGCT	5157		
QY	1135	CAATCGTCTGAATGGGATTTTACATTTGGCAGATTACACAGTACACGACGAGTAATAA	1194		
Db	5156	CAATCGTCTGAATGGGATTTTACATTTGGCAGATTACACAGTACACGACGAGTAATAA	5097		
QY	1195	AAGGACATTCGCGCAACAGAG	1217		
Db	5096	AAGGACATTCGCGCAACAGAG	5074		
RESULT 13					
SYNTG130V/C					
LOCUS	SYNTG130V	7265 bp	DNA	circular	SYN 26-JUL-1993
DEFINITION	M13tg130 phage cloning vector.				
ACCESSION	L08828				
VERSION	L08828.1	GI:310852			
KEYWORDS					
SOURCE	Synthetic construct DNA.				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 7265)				
AUTHORS	Gilbert,W				
TITLE	Obtained from VecBase 3.0				
JOURNAL	Unpublished (1991)				
COMMENT	These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program.				
	M13tg130 - Phage Cloning Vector				
	ENTRY M13tg130				#TYPE DNA CIRCULAR TITLE M13tg130
	- Phage Cloning Vector				
	DATE 19-DEC-1986				
	ACCESSION VB0054				
	SOURCE artificial				
	REFERENCE				
	#number 1				
	#authors Kieny M.P., Lathe R., Lecocq J.P.				
	#journal Gene (1983) 26: 91-99				
	REFERENCE				
	#number 2				
	#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.				
	#book Cloning Vectors, Elsevier 1985 and supplements				
	#comment vector I-A-v-1				
	COMMENT				
	Assembled from M13mp7 and M13tg130-Polylinker by F. Pfeiffer				
	KEYWORDS				
	CROSSREFERENCE				
	#parent				
	VecBase(3):M13mp7, GenBank(50):M13tg130,				
	VecSource(3):bGal130				
	#brother				
	VecBase(3):M13tg131				
	#offspring				
	VecBase(3):pUC830, VecBase(3):pOM2, VecBase(3):pOM4,				
	VecBase(3):pOM8				
	PARENT				
	Features of M13tg130 (7265 bp)				
	residue				
	1-6230	1-6230 M13mp7			
	6231-6299	1- 69 M13tg130-Polylinker			
	6300-7265	6273-7238 M13mp7			
	Conflict (cfl) and Mutations (mut): none				
	FEATURE				
	POLYLINKER				
	ECORI-SmaI-SacI-EcoRV-SphI-KpnI-XbaI-HindIII-BamHI-SalI-PstI				
	SELECTION				
	#indicator beta-galactosidase				
	SUMMARY M13tg130 #length 7265 #checksum 2344.				
	Location/Qualifiers				
	FEATURES				

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source 1. .7265
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1774 a 1541 c 1535 g 2415 t
ORIGIN

Query Match 95.4%; Score 1161.4; DB 12: Length 7265;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 GAATTCGTAATCATAGTGTATAGCTGTTTCTCTGTGTGAATTTGTTATCCCGTCACAATTC 114
Db 6236 GAATTCGTAATCATAGTGTATAGCTGTTTCTCTGTGTGAATTTGTTATCCCGTCACAATTC 6177

QY 115 ACACACATACGAGCCGGAAGCAATAAGTGTAAAGCTGTGGGTGCCTAATGAGTGAGCTA 174
Db 6176 ACACACATACGAGCCGGAAGCAATAAGTGTAAAGCTGTGGGTGCCTAATGAGTGAGCTA 6117

QY 175 ACTCACAATAATTTGGTTCGGCTCAGTCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 234
Db 6116 ACTCACAATAATTTGGTTCGGCTCAGTCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 6057

QY 235 GCTGCATTAAATGAATCGGCAACGGCGGAGAGCGGTGTTGCGTATTTGGGCGCCAGG 294
Db 6056 GCTGCATTAAATGAATCGGCAACGGCGGAGAGCGGTGTTGCGTATTTGGGCGCCAGG 5997

QY 295 TGGTTTCTTTTCCAGTGTAGAGCGGCAACAGCTGATTGTCCTTTACCGCTGGCCCT 354
Db 5996 TGGTTTCTTTTCCAGTGTAGAGCGGCAACAGCTGATTGTCCTTTACCGCTGGCCCT 5937

QY 355 GAGAGAGTTGACGAGCGGTCCAGCTGTTTCCGAGAGCGGCAAAATCCTGTTTGA 414
Db 5936 GAGAGAGTTGACGAGCGGTCCAGCTGTTTCCGAGAGCGGCAAAATCCTGTTTGA 5877

QY 415 TGGTGTTCGGAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGT 474
Db 5876 TGGTGTTCGGAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGT 5817

QY 475 GAGTGTCTTCCAGTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCAACGTCAA 534
Db 5816 GAGTGTCTTCCAGTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCAACGTCAA 5757

QY 535 AGGCGGAAACCGTCTATCAGGCGATGCGCCACTAGTGAACCATCACCCAAATCAAG 594
Db 5756 AGGCGGAAACCGTCTATCAGGCGATGCGCCACTAGTGAACCATCACCCAAATCAAG 5697

QY 595 TTTTTCGGGTGCGAGGTCCGTAAAGCACTAAATCGGAACCTTAAGGAGCCCGCGATT 654
Db 5696 TTTTTCGGGTGCGAGGTCCGTAAAGCACTAAATCGGAACCTTAAGGAGCCCGCGATT 5637

QY 655 TAGAGCTTGACGGGAAAGCCGGCAACGTGGCGAGAAAGGAGGAGAAAGCGAAAGG 714
Db 5636 TAGAGCTTGACGGGAAAGCCGGCAACGTGGCGAGAAAGGAGGAGAAAGCGAAAGG 5577

QY 715 AGCGGGCGCTAGGCGCTGCGAAGTGTAGCGGTGTCGCTGCGCTAACCCACACCCCG 774
Db 5576 AGCGGGCGCTAGGCGCTGCGAAGTGTAGCGGTGTCGCTGCGCTAACCCACACCCCG 5517

QY 775 CGCGCTTAATCGCGCTACAGGCGCGTACTATGTTGCTTTCACAGACAGTATAAG 834
Db 5516 CGCGCTTAATCGCGCTACAGGCGCGTACTATGTTGCTTTCACAGACAGTATAAG 5457

QY 835 TGTCTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAAGGGATTATTAG 894
Db 5456 TGTCTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAAGGGATTATTAG 5397

QY 895 ACAGGAACGCTACGCGAGAACTTTGAGAGTGTTTTATATCAGTACGAGCCACCGAGTA 954
Db 5396 ACAGGAACGCTACGCGAGAACTTTGAGAGTGTTTTATATCAGTACGAGCCACCGAGTA 5337

QY 955 AAAGAGTCTGTCCATCACGCAAAATTAACCGTTGTAGCAATACCTTTGATTAGTAATAA 1014
Db 955 AAAGAGTCTGTCCATCACGCAAAATTAACCGTTGTAGCAATACCTTTGATTAGTAATAA 1014

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QY 1015 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGCCCTTGCTGGTAAATATCAGAACAA 1074
Db 5276 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGCCCTTGCTGGTAAATATCAGAACAA 5217
QY 1075 TATTACGCCAGCCATTCACACAGAAACCGCTCATGGAATACCTACATTTTGACGCT 1134
Db 5216 TATTACGCCAGCCATTCACACAGAAACCGCTCATGGAATACCTACATTTTGACGCT 5157
QY 1135 CAATCGTCTGAAATGGATTATTATTCATTTGGCAGATTCCACGACGACCAAGTAATAA 1194
Db 5156 CAATCGTCTGAAATGGATTATTATTCATTTGGCAGATTCCACGACGACCAAGTAATAA 5097
QY 1195 AAGGACATTTCTGCCCAACAGAG 1217
Db 5096 AAGGACATTTCTGCCCAACAGAG 5074

RESULT 14
SYNM13MP1V/c SYNM13MP1V 7196 bp DNA circular SYN 26-JUL-1993
LOCUS M13mpl1 phage cloning vector.
DEFINITION L08813
ACCESSION L08813.1 GI:310750
VERSION L08813.1
KEYWORDS Synthetic construct DNA.
SOURCE Synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 7196)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mpl1
- Phage cloning vector
ENTRY M13MP1 #TYPE DNA CIRCULAR TITLE M13mpl1 -
Phage cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION V00011
SOURCE artificial
REFERENCE
#number 1
#authors Messing J., Gronenborn B., Mueller-Hill B.,
Hofschneider P.H.
#journal Proc. Nat. Acad. Sci. USA (1977) 74: 3642-3646
REFERENCE
#number 2
#authors Dotto G.P., Zinder N.D.
#journal Nature (1984) 311: 279-280
#comment mutation: T at pos 6914, G at pos 6125 in M13 wildtype
COMMENT
Assembled from M13mp2
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
GenBank(50):M13, GenBank(50):EcoLac
#offspring
VecBase(3):M13mp2
PARENT
Features of M13mpl1 (7196 bp)
residue source
1-5868 1-5868 phage M13
5869-6657 936-1724 Lac-Operon
6658-7196 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mpl1 source
cfl 5977 G A 1044 Lac
cfl 6468 G T 1535 Lac
mut 6914 T G 6125 phage M13
```

Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene v.
FEATURE
POLYLINKER none
SELECTION
#Indicator beta-galactosidase
SUMMARY M13mpl #length 7196 #checksum 3865.
Location/Qualifiers
1. 7196
/organism="synthetic construct"
/db_xref="taxon:32630"
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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1161; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 GAATTCGTAATCATGGTCTAGCTCTTCCCTGTGAAATTCCTATCCGCTCACAATTC 114
DB 6236 GAATTCGTAATCATGGTCTAGCTCTTCCCTGTGAAATTCCTATCCGCTCACAATTC 6177
QY 115 ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCCTGGGCTGCTAATGAGTACGCTA 174
DB 6176 ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCCTGGGCTGCTAATGAGTACGCTA 6117
QY 175 ACTACATTAATTCGCTTCCGCTCACTGCCGCTTCCAGTCGGGAACCTGCTGTGCA 234
DB 6116 ACTACATTAATTCGCTTCCGCTCACTGCCGCTTCCAGTCGGGAACCTGCTGTGCA 6057
QY 235 GCTGCATTAATGAATCGGCAACCGCGGGGAGAGCGGTTCGCTATTGGGCGCCAGGG 294
DB 6056 GCTGCATTAATGAATCGGCAACCGCGGGGAGAGCGGTTCGCTATTGGGCGCCAGGG 5997
QY 295 TGGTTTTCCTTTTCCAGCGTACGAGCGGCAACAGCTGATTCGCTTCCAGCGCTGCCCT 354
DB 5996 TGGTTTTCCTTTTCCAGCGTACGAGCGGCAACAGCTGATTCGCTTCCAGCGCTGCCCT 5937
QY 355 GAGAGAGTTCGCAACGCGTCCAGCTGTTGCCCGCAGCGGCAACATCCCTGTTTGA 414
DB 5936 GAGAGAGTTCGCAACGCGTCCAGCTGTTGCCCGCAGCGGCAACATCCCTGTTTGA 5877
QY 415 TGGTGGTTCGAAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGAGTAGGTT 474
DB 5876 TGGTGGTTCGAAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGAGTAGGTT 5817
QY 475 GAGTGTGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGAGTCCCAACGTC 534
DB 5816 GAGTGTGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGAGTCCCAACGTC 5757
QY 535 AGGCGGAAACCCGCTTATCAGGGCGATGGCCGCTAGCTGACCATCACCACCAATCAAG 594
DB 5756 AGGCGGAAACCCGCTTATCAGGGCGATGGCCGCTAGCTGACCATCACCACCAATCAAG 5697
QY 595 TTTTGGGCTGAGGTCGCTTAAGACCTAAATCGGAACCTTAAGGAGGAGCCCGGATT 654
DB 5696 TTTTGGGCTGAGGTCGCTTAAGACCTAAATCGGAACCTTAAGGAGGAGCCCGGATT 5637
QY 655 TAGAGCTTCAGCGGGAAGCCGCAACGTCGCGGAGAAAGGAGGAGAAAGCAAGG 714
DB 5636 TAGAGCTTCAGCGGGAAGCCGCAACGTCGCGGAGAAAGGAGGAGAAAGCAAGG 5577
QY 715 AGCGGCGCTAGGGCGCTGGCAAGTGTACCGCTCAGCTGCGCGTAACCAACACACCGCG 774
DB 5576 AGCGGCGCTAGGGCGCTGGCAAGTGTACCGCTCAGCTGCGCGTAACCAACACACCGCG 5517
QY 775 CGCGCTTAATGGCGCTACAGGCGCGTACTATGTTGCTTTGACGACGATATAAG 834
DB 5516 CGCGCTTAATGGCGCTACAGGCGCGTACTATGTTGCTTTGACGACGATATAAG 5457
QY 835 TGCTTTCCTGTTTGAATCAGAGCGGAGCTAAACAGGAGGCGGATTAAGGATTTAG 894

DB 5456 TGCTTTCCTGTTTGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGATTTAG 5397
QY 895 ACAGGAACGCTAGCCGAGAAATCTTGAGAGTGTGTTTTTAATCAGTGAGCCACCGASTA 954
DB 5396 ACAGGAACGCTAGCCGAGAAATCTTGAGAGTGTGTTTTTAATCAGTGAGCCACCGASTA 5337
QY 955 AAAGAGTCTGCTCATTACGCAAAATTAACCCCTTGTAGCAATACTCTTTGATTAGTAATA 1014
DB 5336 AAAGAGTCTGCTCATTACGCAAAATTAACCCCTTGTAGCAATACTCTTTGATTAGTAATA 5277
QY 1015 CATCAGTCTGCTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACAA 1074
DB 5276 CATCAGTCTGCTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACAA 5217
QY 1075 TATTACCGCCAGCCATTGCAACAGGAAAGGCTCATGGAATACCTTACATTTTGACGCT 1134
DB 5216 TATTACCGCCAGCCATTGCAACAGGAAAGGCTCATGGAATACCTTACATTTTGACGCT 5157
QY 1135 CAATCGTCTGAAATGGATTTATTTACATTTGGCAGATTCACAGTCACAGGACGATTAATA 1194
DB 5156 CAATCGTCTGAAATGGATTTATTTACATTTGGCAGATTCACAGTCACAGGACGATTAATA 5097
QY 1195 AAGGACATTTCTGGCCAAACAGAG 1217
DB 5096 AAGGACATTTCTGGCCAAACAGAG 5074

RESULT 15
SYNTG131V/c SYNTG131V 7265 bp DNA circular SYN 26-JUL-1993
LOCUS M13tg131 phage cloning vector.
DEFINITION L08833
ACCESSION L08833.1 GI:310853
VERSION
KEYWORDS Synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 7265)
AUTHORS Gilbert, W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program.
M13tg131 - Phage Cloning Vector #TYPE DNA CIRCULAR TITLE M13tg131
ENTRY M13TG131
DATE 19-DEC-1986
ACCESSION V80055
SOURCE artificial
REFERENCE
#number 1
#authors Kieny M.P., Lathe R., Lecoq J.P.
#Journal Gene (1983) 26: 91-99
REFERENCE
#number 2
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I A-v-1
COMMENT Assembled from M13mp7 and M13tg131-Polylinker by F. Pfeiffer
COMMENT The BglII site in the polylinker region is not unique. KEYWORDS
CROSSREFERENCE
#parent
Vecbase(3):M13mp7, GenBank(50):M13tg131,
VecSource(3):bgall31
#brother
Vecbase(3):M13tg130
#offspring
Vecbase(3):pUC931, VecBase(3):pOM1, VecBase(3):pOM3,
VecBase(3):pOM9
PARENT

Features of M13tg131 (7265 bp)
residue source
1-6232 1-6232 M13mp7
6233-6305 1- 73 M13tg131-Polylinker
6306-7265 6279-7238 M13mp7
Conflict (cfl) and Mutations (mut): none
FEATURE
POLYLINKER (BglII)-PstI-SalI-BamHI-HindIII-XbaI-
KpnI-SphI-EcoRV-SstI-SmaI-EcoRI
SELECTION
#indicator beta-galactosidase
SUMMARY M13tg131 #length 7265 #checksum 2704.
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1772 a 1543 c 1534 g 2416 t
ORIGIN

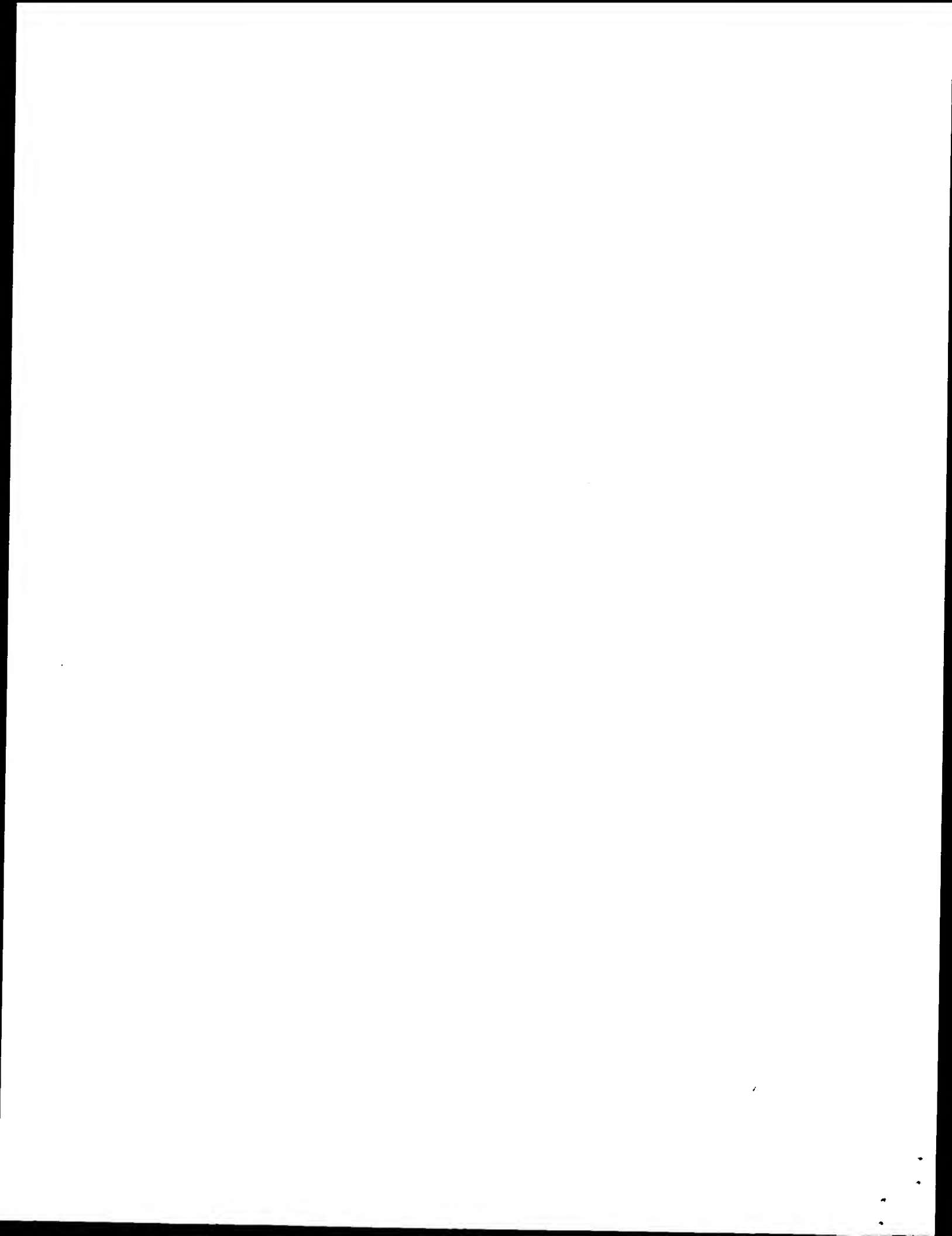
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1158; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 TTCGTAATCATGTCATAGTGTTCCTGTGTGAATTTGTTATCCGCTCAATTCACA 117
DB 6233 TGCCTAATCATGTCATAGTGTTCCTGTGTGAATTTGTTATCCGCTCAATTCACA 6174
QY 118 CAACATACAGCGGAGGAGGATTAAGCTGGGTGCCTAATAGTGAGCTAACT 177
DB 6173 CAACATACAGCGGAGGAGGATTAAGCTGGGTGCCTAATAGTGAGCTAACT 6114
QY 178 CACATTAATGTCGCTGCTACTGCGCCCTTCCAGTCGGGAAACCTGCTGCGCAGCT 237
DB 6113 CACATTAATGTCGCTGCTACTGCGCCCTTCCAGTCGGGAAACCTGCTGCGCAGCT 6054
QY 238 GCATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTCGCTATTGGCGCGCAGGGTGG 297
DB 6053 GCATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTCGCTATTGGCGCGCAGGGTGG 5994
QY 298 TTTTCTTTTCCAGTGGAGCGGCAACAGCTGATTCGCCCTTCACCGGCTGGCCCTGAG 357
DB 5993 TTTTCTTTTCCAGTGGAGCGGCAACAGCTGATTCGCCCTTCACCGGCTGGCCCTGAG 5934
QY 358 AGAGTTCGAGCAAGGGTCCAGCTGGTTTCCCGCAGCGGCAAAATCCCTGTTGATGG 417
DB 5933 AGAGTTCGAGCAAGGGTCCAGCTGGTTTCCCGCAGCGGCAAAATCCCTGTTGATGG 5874
QY 418 TGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAG 477
DB 5873 TGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAG 5814
QY 478 TGTGTTCCAGTTPGGAACAGAGTCCACTATTAAAGAACGTTGACCTCCCAACGTCAAAG 537
DB 5813 TGTGTTCCAGTTPGGAACAGAGTCCACTATTAAAGAACGTTGACCTCCCAACGTCAAAG 5754
QY 538 GCGAAAACCGCTCTATCAGGCGGATGCCACCTACGTTGACCTACCCCAATCAAGTTT 597
DB 5753 GCGAAAACCGCTCTATCAGGCGGATGCCACCTACGTTGACCTACCCCAATCAAGTTT 5694
QY 598 TTTGGGGTCCAGTGGCGGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCGATTTAG 657
DB 5693 TTTGGGGTCCAGTGGCGGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCGATTTAG 5634
QY 658 AGCTTCAGGGGAAACCGCGACGTGGCGGAAAGGAGGAAAGAAAGCGAAAGGAGC 717
DB 5633 AGCTTCAGGGGAAACCGCGACGTGGCGGAAAGGAGGAAAGAAAGCGAAAGGAGC 5574
QY 718 GGGCGCTAGGGCGCTGGCAAGTGTAGCGTTCAGCTGCGGTAAACCAACACCCCGCC 777
DB 5573 GGGCGCTAGGGCGCTGGCAAGTGTAGCGTTCAGCTGCGGTAAACCAACACCCCGCC 5514
QY 778 GCTTAATGCGCGCTACAGGGCGGCTACTATGTTGCTTTGACGACGATTAACGTCG 837

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Job time: 6593 sec

us-10-014-743-1.rge

Thu Aug 1 12:08:38 2002



Thu Aug 1 12:08:39 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:44:44 ; Search time 365.16 seconds
(without alignments)
5722.108 Million cell updates/sec

Title: us-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAGCTTGCATGCTGCA.....GGACATTTCTGCCAACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1217	100.0	1217	18 AAV12871	M13 DNA sequence.
2	1217	100.0	1217	20 AAZ09714	Bacteriophage M13
3	1217	100.0	1217	20 AAX99692	M13 DNA sequence u
4	1165.2	95.7	9955	9 AAN81542	Sequence of mcp1-2
5	1165.2	95.7	9955	11 AAQ05877	mgp1-2 plasmid seq
6	1165.2	95.7	9955	13 AAQ031625	Right-half vector
7	1150.8	94.6	7294	15 AAQ66626	Right-half vector
8	1150.8	94.6	7294	15 AAQ66630	M13IX421. Synthet
9	1147.6	94.3	7294	13 AAQ24174	

c 10	1144.4	94.0	7294	13	AAQ24170	M13IX42. Synthet
c 11	1141	93.8	7300	22	AAF59234	M13mp18 nucleotide
c 12	1140.4	93.7	7084	21	AAZ51028	Modified filament
c 13	1131.4	93.0	7317	19	AAV03651	M13-based vector M
c 14	1131.4	93.0	7317	20	AAZ16953	Plasmid M13IX11.
c 15	1131.4	93.0	7317	21	AAZ16953	Kappa light chain
c 16	1131.4	93.0	7320	15	AAQ66627	Left-half vector M
c 17	1131.4	93.0	7557	19	AAV03653	M13-based vector M
c 18	1131.4	93.0	7557	20	AAZ16961	Plasmid M13IX13.
c 19	1131.4	93.0	7557	21	AAZ91527	Nucleotide sequenc
c 20	1131.4	93.0	8118	19	AAV03654	M13-based vector M
c 21	1131.4	93.0	8118	21	AAZ91528	Plasmid M13IX60.
c 22	1131.4	93.0	8118	21	AAZ91528	Nucleotide sequenc
c 23	1131	92.9	7394	15	AAQ66631	Left-half vector M
c 24	1131	92.9	7409	15	AAQ66629	Vector M13IX30 for
c 25	1131	92.9	7445	15	AAQ66628	M13-based vector M
c 26	1131	92.9	7445	19	AAV03650	Plasmid M13IX30.
c 27	1131	92.9	7445	21	AAZ16937	Heavy chain Fd lib
c 28	1131	92.9	7729	19	AAV03652	M13-based vector M
c 29	1131	92.9	7729	20	AAZ16959	Plasmid M13IX34.
c 30	1131	92.9	7729	21	AAZ91526	Nucleotide sequenc
c 31	1131	92.8	7394	13	AAQ24175	M13ED04. Syntheti
c 32	1129.4	92.5	7445	13	AAQ24172	M13IX30. Syntheti
c 33	1126.2	92.2	7320	13	AAQ24173	M13IX22. Syntheti
c 34	1121.8	92.1	7409	13	AAQ24173	M13IXD03. Synthet
c 35	1121.4	92.1	7409	13	AAQ24173	M13mp18 sense stra
c 36	1030.4	84.7	1050	14	AAQ46689	Sequencing vector
c 37	845.8	69.6	7652	14	AAQ46682	Sequence of phage
c 38	754	62.0	6971	20	AAZ26304	Sequence of phage
c 39	739.6	60.8	7055	20	AAZ26303	Chimeric adeno-ass
c 40	739.6	60.8	7783	20	AAZ26302	Chimeric adeno-ass
c 41	716.4	58.9	8151	21	AAQ00832	Plasmid pAV CMVlac
c 42	716.4	58.9	8178	21	AAQ00834	AV.CMVlac2 cis pla
c 43	716.4	58.9	8509	18	AAT59271	Second generation
c 44	716.4	58.9	8509	20	AAZ33862	
c 45	715.4	58.8	8299	18	AAT59273	

ALIGNMENTS

RESULT 1
AAV12871 standard; DNA; 1217 BP.

XX AAV12871;

XX 14-MAY-1998 (first entry)

XX M13 DNA sequence.

XX Energy transfer dye; donor dye; acceptor dye; oligonucleotide labelling;
XX nucleic acid sequencing; fluorescence intensity; M13; ss.

XX Synthetic.

XX EP805190-A2.

XX 05-NOV-1997.

XX 02-MAY-1997; 97EP-0303039.

XX 04-OCT-1996; 96US-0726462.

XX 03-MAY-1996; 96US-0642330.

XX (PEKE) PERKIN-ELMER CORP.

XX Lee LG, Rosenblum B, Spurgeon SL;

XX WPI; 1997-529051/49.

XX Fluorescent energy transfer dyes - useful for labelling
XX dideoxynucleotides, oligonucleotides, etc.

XX
PS
XX

Example 5; Page 54-55; 79pp; English.

This sequence represents the M13 sequence identified using the primer shown in AAV12871 labelled with a dye of the invention. The dye is an energy transfer dye of formula D-R21-Z1-CO-R22-R28-A (1), where: D is a donor dye that absorbs light at a first wavelength and emits excitation energy in response; A is an acceptor dye that absorbs the excitation energy from D and fluoresces at a second wavelength in response; Z1 = NH, S or O; R21 = 1-5C alkylene; R22 = an alkene, diene or alkene group, an unsaturated 5- or 6-membered ring or a fused ring structure; R28 = a group which includes a functionality to attach the linker to the acceptor dye. R28 is especially R29-Z2-CO, where R29 = 1-5C alkylene and Z2 = NH, S or O. The dyes are used for labelling nucleosides, nucleoside mono-, di- and triphosphates, oligonucleotides and oligonucleotide analogues, especially for labelling oligonucleotide primers or didoxynucleotides used for nucleic acid sequencing. The dyes give greater fluorescence intensities than the acceptor dyes alone.

Sequence 1217 BP; 335 A; 291 C; 321 G; 270 T; 0 other;

Query Match 100.0%; Score 1217; DB 18; Length 1217;
Best Local Similarity 100.0%; Pred. No. 8.2e-221;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GCCAAGCTTGCATGCTGCGAGTTCGACTAGAGATCCCGGGTACCGAGCTCGAATTC 60
   |||
Db 1 gccaaagctgcatgctgctgagctgagctagagatcccggtaccgagctcgaaattc 60

QY 61 GTAATCATGGTCATAGCTGTTCTCTGTGTAATGTTATTCGCTCACAAATCCACACAA 120
   |||
Db 61 gtaatcatgctgcatgctgctgagctgagctgagctgagctgagctgagctgagctgag 120

QY 121 CATAGAGCGGGAAGCATAAAGTGAAGCTGGGGTGCCTAATGAGTGAAGTCACTAC 180
   |||
Db 121 catagagcgaggagcacaataagtgaaagcctgggtgctgctgagctgagctgagctgag 180

QY 181 ATTAATTCGGTTCGCTCAGTCCCGCTTCCAGTCCGGAACCTGCTGCGACGCTGCA 240
   |||
Db 181 attaatttcggttcgctcagctccgcttccagtcgggaaacctgctgctgagctgagctg 240

QY 241 TTAATGAATCGCCACGCGGGGAGAGGGGTTGCTGTTGGCGCGCAGGGTGGTTT 300
   |||
Db 241 ttaatgaatcgccacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300

QY 301 TTCTTTTCCACAGTGAGACGCGCAACAGCTGATTCGCTTCCAGTCCGCGCTGAGAGA 360
   |||
Db 301 ttcttttccacagtgagacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360

QY 361 GTTGCACGACGGTCCACGCTGTTTGGCCCGCAGCGCAAAATCCCTGTTGATGGTGG 420
   |||
Db 361 gttgcacgacgggtccacgctgcttggcccgagcagcgcaaaatccctgttggatggtgg 420

QY 421 TTCGAAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGGTGGTGGT 480
   |||
Db 421 ttcgaaatcgggcaaaatcccttataatcaaaagatagcccgagataggggtgggtgggt 480

QY 481 TGTTCAGTTTGGACAGAGTCCACTATTAAAGAACGTGACCTCCCAACGTCAAGAGCGG 540
   |||
Db 481 tgttcagtttggacagagtgctcactattaaagaaagcgtgactcccaacgtcaaaagggcg 540

QY 541 AAAAACCGTCTATCAGGGCGATGGCCACCTACCTGACCTGACCTGACCTGACCTGAC 600
   |||
Db 541 aaaaacgctctacagggcgatggccacacctacctgacctgacctgacctgacctgacctg 600

QY 601 GGGGTGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGGATTTAGAGC 660
   |||
Db 601 ggggtgaggtgctgtaagcactaaatcggaacaccttaagagagcgcccgatcttagagc 660

QY 661 TTGACGGGGAAGCGCGCAAGCTGCGGAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAG 720
   |||
Db 661 ttgacggggaagcgcgcaagctgctgagagagagagagagagagagagagagagagagag 720

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QY 721 CGCTAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGCGTAAACACACACACCGCGCGCT 780
   |||
Db 721 cgctagggcgctgcgcaagtgtagcgtgctgctgctgctgctgctgctgctgctgctgct 780

QY 781 TAATGCGCGCTACAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
   |||
Db 781 taatgcgcgctacagggcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 840

QY 841 CCTGCTGCAATCAGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
   |||
Db 841 cctgctgcaatcagacgcgcgctgctgctgctgctgctgctgctgctgctgctgctgctg 900

QY 901 AGGTACGCGCGCAATCTTCTGAGAGTCTTCTGAGAGTCTTCTGAGAGTCTTCTGAGAG 960
   |||
Db 901 acggtacgcgcaatcctgagagtgctgctgctgctgctgctgctgctgctgctgctgctg 960

QY 961 TCTGCTGCTGCAATCAGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
   |||
Db 961 tctgctgctgcaatcagacgcgcgctgctgctgctgctgctgctgctgctgctgctgctg 1020

QY 1021 TTGCTGCTGCTGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
   |||
Db 1021 ttgctgctgctgagagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1080

QY 1081 CGCCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
   |||
Db 1081 cgccagcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1140

QY 1141 TCTGAAATGGAATTTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
   |||
Db 1141 tctgaaatggaaatTTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200

QY 1201 CATTGCTGCGCAACAGAG 1217
   |||
Db 1201 cattctggccaacagag 1217

```

RESULT 2

AAZ09714
ID AAZ09714 standard; DNA; 1217 BP.

AC AAZ09714;

XX 15-NOV-1999 (first entry)

DE Bacteriophage M13 DNA fragment.

XX Energy transfer dye; fluorescence; donor; acceptor; excitation energy;
XX light absorption; nucleic acid sequencing; detection; fluorophore; ss.
OS Bacteriophage m13.

PN US5945526-A.

XX 31-AUG-1999.

XX 23-MAR-1998; 98US-0046203.

XX 23-MAR-1998; 98US-0046203.

XX 03-MAY-1996; 96US-0642330.

XX 27-JUN-1996; 96US-0672196.

XX (PEKE) PERKIN-ELMER CORP.

PI Lee LG, Rosenblum B, Spurgeon SL;

XX WPI; 1999-550120/46.

XX New energy transfer dye, used in nucleic acid sequencing

PS Disclosure; Column 85-88; 77pp; English.

Query Match 95.7%; Score 1165.2; DB 9; Length 9955:

Db 5223 AGAACAATATTAACCCAGCCATTCACACAGGAAACGCTCATGGAATAACCTACATTT 5164
Qy 1128 TGACGCTCAATCGTCTGAAATGATTTATTTACATTTGGCAGATTCCACGATCACAGCA 1187
Db 5163 TGACGCTCAATCGTCTGAAATGATTTATTTACATTTGGCAGATTCCACGATCACAGCA 5104
Qy 1188 GTAATTAAGGACATTCCTGGCCAAACAGAG 1217
Db 5103 GTAATTAAGGACATTCCTGGCCAAACAGAG 5074

RESULT 5
AAQ05877/C
ID AAQ05877 standard; DNA; 9955 BP.

AC AAQ05877;

XX 10-JAN-1991 (first entry)

DE mgp1-2 plasmid sequence encoding T7 RNA polymerase under the control
DE of a lac promoter.

XX pTrx-2; pGP5-5; mgp1-2; ds.

XX Bacteriophage t7.

XX EP386857-A.

XX 12-SEP-1990.

XX 24-DEC-1987; 87EP-0201138.

XX 07-MAY-1990; 90EP-0201138.

PR 14-JAN-1987; 87US-0003227.

PR 14-DEC-1987; 87US-0132569.

XX (HARD) HARVARD COLLEGE.

PA Tabor S, Richardson CC;

PI WPI; 1990-276890/37.

XX Amplification of DNA sequences - by annealing primers then
XX incubating with T7-type DNA polymerase having reduced
XX exo:nuclease activity.

PS Example 1; Fig 9; 43pp; English.

XX In order to overproduce T7 DNA polymerase in a cellular expression
CC system, the two components, thioredoxin and gene 5 protein must be
CC produced in a one to one ratio.

CC Thioredoxin is cloned into plasmid pTrx-2 under the control of the
CC tac promoter.

CC T7 gene 5 is included in plasmid pGP5-5 under the control of the
CC phi 10 promoter.

CC phi 10 promoter is induced only in the presence of T7 RNA polymerase
CC which is provided by the plasmid mgp1-2 under the influence of the
CC lac promoter.

XX Sequence 9955 BP; 2454 A; 2219 C; 2241 G; 3038 T; 3 other;

Query Match 95.7%; Score 1165.2; DB 11; Length 9955;
Best Local Similarity 99.7%; Pred. No. 4.2e-211;
Matches 1167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 48 CGAGCTCGAATTCGTAATCATGCTGTTCCCTGTGTGTAATTTATTCGCTCA 107
Db 6243 CGAGCTCGAATTCGTAATCATGCTGTTCCCTGTGTGTAATTTATTCGCTCA 6184

Qy 108 CAATTCACACAAACATACGAGCCGGAAGCATAAAGCTGTAAGCCCTGGGTGCTAATGAG 167
Db 6183 CAATTCACACAAACATACGAGCCGGAAGCATAAAGCTGTAAGCCCTGGGTGCTAATGAG 6124

Best Local Similarity 99.7%; Pred. No. 4.2e-211;
Matches 1167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 48 CGAGCTCGAATTCGTAATCATGCTGTTCCCTGTGTGTAATTTATTCGCTCA 107
Db 6243 CGAGCTCGAATTCGTAATCATGCTGTTCCCTGTGTGTAATTTATTCGCTCA 6184

Qy 108 CAATTCACACAAACATACGAGCCGGAAGCATAAAGCTGTAAGCCCTGGGTGCTAATGAG 167
Db 6183 CAATTCACACAAACATACGAGCCGGAAGCATAAAGCTGTAAGCCCTGGGTGCTAATGAG 6124

Qy 168 TGAGCTCACTACATTAATTCGCTTGGCTCACTGCGCCCTTCCAGTCGCGAAACCTGT 227
Db 6123 TGAGCTCACTACATTAATTCGCTTGGCTCACTGCGCCCTTCCAGTCGCGAAACCTGT 6064

Qy 228 CGTCCAGCTGCATTAATGAATCGGCCAAGCGCGGGGAGAGGGGTTGGTATTCGGC 287
Db 6063 CGTCCAGCTGCATTAATGAATCGGCCAAGCGCGGGGAGAGGGGTTGGTATTCGGC 6004

Qy 288 GCCAGGTGGTTTCTTTTCCAGCTGAGACGGGCAACAGCTGATTCGCCCTTCCACCGCC 347
Db 6003 GCCAGGTGGTTTCTTTTCCAGCTGAGACGGGCAACAGCTGATTCGCCCTTCCACCGCC 5944

Qy 348 TGGCCCTGAGAGAGTTGACGAGCGGTCCAGCTGGTTTCCCGCAGCAGCGGAAATCC 407
Db 5943 TGGCCCTGAGAGAGTTGACGAGCGGTCCAGCTGGTTTCCCGCAGCAGCGGAAATCC 5884

Qy 408 TGTTTGATGGTTCGGAATCGGCAAAATCCCTTATTAATCAAAAGATAGCCCGAGA 467
Db 5883 TGTTTGATGGTTCGGAATCGGCAAAATCCCTTATTAATCAAAAGATAGCCCGAGA 5824

Qy 468 TAGGGTTGAGTGTGTTCCAGCTTTGGAACAAGAGTCCACTATTAAGAAGCTGGACTCCA 527
Db 5823 TAGGGTTGAGTGTGTTCCAGCTTTGGAACAAGAGTCCACTATTAAGAAGCTGGACTCCA 5764

Qy 528 ACGTCAAGGGGGAACAAACCGCTATACAGGGGATGGCCCACTACGTGAACCATCACCA 587
Db 5763 ACGTCAAGGGGGAACAAACCGCTATACAGGGGATGGCCCACTACGTGAACCATCACCA 5704

Qy 588 AATCAAGTTTGTGGGTGAGTGCCTGAGTGCCTGAAGCACTAAATCGGAACCCCTAAAGGAGCC 647
Db 5703 AATCAAGTTTGTGGGTGAGTGCCTGAGTGCCTGAAGCACTAAATCGGAACCCCTAAAGGAGCC 5644

Qy 648 CCGGATTTAGAGCTTGACGGGGAAACCGCGCAACCTGCGGAGAAAGGAAGGAAAG 707
Db 5643 CCGGATTTAGAGCTTGACGGGGAAACCGCGCAACCTGCGGAGAAAGGAAGGAAAG 5584

Qy 708 CGAAGAGCGGCGCTAGGCGCTGGAAGTGTAGCGGTGACGCTGCGGTAAACCA 767
Db 5583 CGAAGAGCGGCGCTAGGCGCTGGAAGTGTAGCGGTGACGCTGCGGTAAACCA 5524

Qy 768 CACCGCGCGCTTAATGCGCGCTACAGCGCGGTACTATGTTGCTTTCAGGAGCAGC 827
Db 5523 CACCGCGCGCTTAATGCGCGCTACAGCGCGGTACTATGTTGCTTTCAGGAGCAGC 5464

Qy 828 TATACAGTCTTCTCTGCTGGAATCAGAGCGGGAGCTTAAACAGGAGCCGATTAAGGG 887
Db 5463 TATACAGTCTTCTCTGCTGGAATCAGAGCGGGAGCTTAAACAGGAGCCGATTAAGGG 5404

Qy 888 ATTTTAGACAGGACGGTACGCCAGAACTTTGAGAGTGTGTTTATATCATGAGGCCA 947
Db 5403 ATTTTAGACAGGACGGTACGCCAGAACTTTGAGAGTGTGTTTATATCATGAGGCCA 5344

Qy 948 CCGAGTAAAGAGTCTGTCCATCAGCAAAATTAACCGTTGTAGCAATACTCTTTTGA 1007
Db 5343 CCGAGTAAAGAGTCTGTCCATCAGCAAAATTAACCGTTGTAGCAATACTCTTTTGA 5284

Qy 1008 GTAATTAACATCACTTCCCTGAGTGTAGAGAACTCAAACTATCGGCCCTGCTGTAATATCC 1067
Db 5283 GTAATTAACATCACTTCCCTGAGTGTAGAGAACTCAAACTATCGGCCCTGCTGTAATATCC 5224

Qy 1068 AGAACAAATATTACCGCAGCCATTTGCAACAGGAAACCGCTCATGGAATACCTACATTT 1127
Db 1127 AGAACAAATATTACCGCAGCCATTTGCAACAGGAAACCGCTCATGGAATACCTACATTT 1127

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Qy 408 TGTTGATGGTGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGA 467
Db 5883 TGTTGATGGTGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGA 5824
Qy 468 TAGGTTGAGTGTGTTTCCAGTTTGGAAACAGAGTCCACATATTAAAGAACGTGACTCCA 527
Db 5823 TAGGTTGAGTGTGTTTCCAGTTTGGAAACAGAGTCCACATATTAAAGAACGTGACTCCA 5764
Qy 528 ACGTCAAAAGGGGCAAAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCA 587
Db 5763 ACGTCAAAAGGGGCAAAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCA 5704
Qy 588 AATCAAGTTTGTGGGTTCGAGTCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCC 647
Db 5703 AATCAAGTTTGTGGGTTCGAGTCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCC 5644
Qy 648 CCCGATTTAGAGCTTGTAGCGGGGAAAGCGCGGACGTGGCGAGAAAGGGAAGAAAG 707
Db 5643 CCCGATTTAGAGCTTGTAGCGGGGAAAGCGCGGACGTGGCGAGAAAGGGAAGAAAG 5584
Qy 708 CGAAGGAGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTCAAGTGGCGCTTAACCAACA 767
Db 5583 CGAAGGAGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTCAAGTGGCGCTTAACCAACA 5524
Qy 768 CACCCCGCGCTTAATGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAG 827
Db 5523 CACCCCGCGCTTAATGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAG 5464
Qy 828 TATAAGCTGTTTCCCTGTTGGTGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGG 887
Db 5463 TATAAGCTGTTTCCCTGTTGGTGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGG 5404
Qy 888 ATTTTACAGAGGAGCTAGCGCAGAAATCTTGAGAAAGTGTGTTTATAATCAGTGAGGCA 947
Db 5403 ATTTTACAGAGGAGCTAGCGCAGAAATCTTGAGAAAGTGTGTTTATAATCAGTGAGGCA 5344
Qy 948 CCGAGTAAAGAGTGTGTCATCAGCGAAATTAACCGTGTAGCAATCTCTTTGATTA 1007
Db 5343 CCGAGTAAAGAGTGTGTCATCAGCGAAATTAACCGTGTAGCAATCTCTTTGATTA 5284
Qy 1008 GTAATACATCACTTGGCTCAGTAGAAGAACTCAAACTATCGGCGCTTGTGTAATATCC 1067
Db 5283 GTAATACATCACTTGGCTCAGTAGAAGAACTCAAACTATCGGCGCTTGTGTAATATCC 5224
Qy 1068 AGAACAATATTACCGCCAGCCATTTGCAACAGGAAACGGCTCATGGAAATACCTACATTT 1127
Db 5223 AGAACAATATTACCGCCAGCCATTTGCAACAGGAAACGGCTCATGGAAATACCTACATTT 5164
Qy 1128 TGAGCTCAATCGTCTGAATGGATTTTATACATTTGGCAGATTCACCAGTCAACAGCA 1187
Db 5163 TGAGCTCAATCGTCTGAATGGATTTTATACATTTGGCAGATTCACCAGTCAACAGCA 5104
Qy 1188 GTAATAAAGGAGACATTTGCGCCACAGAG 1217
Db 5103 GTAATAAAGGAGACATTTGCGCCACAGAG 5074
RESULT 7
ID AAQ66626/c
XX AAQ66626 standard; DNA; 7294 BP.
AC AAQ66626;
XX
DT 20-JAN-1995 (first entry)
XX
DE Right-half vector M13IX42.
XX
KW vector M13IX42; right-half vector; randomised oligonucleotides;
KW surface expression; random peptide; constrained secondary structure;
KW pseudo wild-type M13 gene VIII; ds.
XX
OS Synthetic.

XX WO9411496-A.
XX 26-MAY-1994.
XX 09-NOV-1993; 93WO-US10850.
XX 10-NOV-1992; 92US-0978893.
XX (IXSY-) IXSYS INC.
XX Huse WD;
XX WPI; 1994-183498/22.
XX Cells expressing oligo:nucleotide(s) having random codon
XX sequences - are used for producing soluble peptide(s) having a
XX constrained secondary structure in soln.
XX Example 1: Page 78-82; 152pp; English.
XX M13IX42 was constructed to harbour the right-half populations of
XX randomised oligonucleotides. M13mp8 was the starting vector which
XX was modified to contain, in addition to the encoded wild-type M13
XX gene VIII all ready present in the vector: a pseudo-wild-type M13
XX gene VIII sequence with a stop codon placed between it and an EcoRI-
XX SacI cloning site for randomised oligonucleotides; a pair of PstI
XX sites to be used for joining with M13IX22, the left-hand vector; a
XX second stop codon placed on the opposite side of the vector than the
XX portion being combined with the left-half vector; and various other
XX mutations to remove redundant restriction sites and the N-terminal
XX portion of LacZ.
XX Sequence 7294 BP; 1787 A; 1528 C; 1532 G; 2427 T; 0 other;
SQ
Query Match 94.6%; Score 1150.8; DB 15; Length 7294;
Best Local Similarity 99.8%; Pred. No. 2.2e-208;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 64 ATCATGTCATAGCTGTTTCCCTGTTGAAATTTGTTATCGCTCAAAATTTCCACACAAAT 123
Db 6226 ATCTGTCATAGCTGTTTCCCTGTTGAAATTTGTTATCGCTCAAAATTTCCACACAAAT 6167
Qy 124 ACGAGCGGAAGCATAAAGTGTAAAGCTGTGGGTGCTTAATGAGTCACTCACTACATT 183
Db 6166 ACGAGCGGAAGCATAAAGTGTAAAGCTGTGGGTGCTTAATGAGTCACTCACTACATT 6107
Qy 184 AATTGCGTTCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCGAGTGCATTA 243
Db 6106 AATTGCGTTCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCGAGTGCATTA 6047
Qy 244 ATGAATCGGCAACGCGCGGAGAGCGGTTTGGCGTATTGGGCGCAGGTTTTC 303
Db 6046 ATGAATCGGCAACGCGCGGAGAGCGGTTTGGCGTATTGGGCGCAGGTTTTC 5987
Qy 304 TTTTTCACGAGTGAGCGGCAACAGCTGATTGCGCTTTCACCGCTGCGCTGAGAGATT 363
Db 5986 TTTTTCACGAGTGAGCGGCAACAGCTGATTGCGCTTTCACCGCTGCGCTGAGAGATT 5927
Qy 364 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGCGGAAATCTCTGTTGATGTTGTTTC 423
Db 5926 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGCGGAAATCTCTGTTGATGTTGTTTC 5867
Qy 424 CGAATCGGCAAAATCTCTTATTAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
Db 5866 CGAATCGGCAAAATCTCTTATTAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
Qy 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGAGCTCCAAACGTCAAGGCGGAAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGAGCTCCAAACGTCAAGGCGGAAA 5747
Qy 544 AACCGTCTATAGCGCGGATGCGCCCACTACGTTGAACCATCACCCCAANTCAAGTTTTTTGGG 603

XX	
PI	Huse WD;
XX	
XX	WPI; 1994-183498/22.
XX	
XX	Cells expressing oligo:nucleotide(s) having random codon
PT	sequences - are used for producing soluble peptide(s) having a
PT	constrained secondary structure in soln.
XX	
XX	Example 3; Page 94-97; 152pp; English.
PS	
XX	
CC	M13IX421 is identical to vector M13IX42 (AAQ66626) except that the
CC	amber codon between the EcoRT-SacI cloning site and the pseudo-wild
CC	type gene VIII sequence was removed. this change ensures that all
CC	expression off the LacZ promoter produces a peptide-gene VIII
CC	fusion protein. The vector was used for the construction of right
CC	half oligonucleotide libraries.
CC	
XX	
XX	Sequence 7294 BP; 1787 A; 1528 C; 1553 G; 2436 T; 0 other;
SQ	

Query Match	94.6%;	Score 1150.8;	DB 15;	Length 7294;
Best Local Similarity	99.8%;	Pred. NO. 2.2e-208;		
Matches 1152; Conservative	0;	Mismatches 2;	Indels 0;	Cons

QY	64	AT	ATCGTGCATAGCTGCTTTCCCTGTGTGAAATGTTATCCGCTCACAAATTCACACAAAT	123
Db	6226	AT	CCCTGCTCATAGCTGCTTTCCCTGTGTGAAATGTTATCCGCTCACAAATTCACACAAAT	616
QY	124	ACG	ACCGCGGAAGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTACATTT	183
Db	6166	ACG	ACGCGCGGAAGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTACATTT	6107
QY	184	AAT	TGCTTGCCTCCTCACTCCCGCTTTCCAGTCGGGAACCTGCTGTCGCCAGCTGCATTA	243
Db	6106	AAT	TGCTTGCCTCCTCACTCCCGCTTTCCAGTCGGGAACCTGCTGTCGCCAGCTGCATTA	6047
QY	244	ATG	AAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCAAGGCTGGTTTTC	303
Db	6046	ATG	AAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCCCAAGGCTGGTTTTC	598
QY	304	TTT	TCCACAGTGAGACGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGATT	363
Db	5986	TTT	TCCACAGTGAGACGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGATT	5927
QY	364	GC	AGCAACGGCTCCACGCTGCTTTGCCCGCAGCGCAAAATCCTGTTGATGGTGCTC	423
Db	5926	GC	AGCAACGGCTCCACGCTGCTTTGCCCGCAGCGCAAAATCCTGTTGATGGTGCTC	5867
QY	424	CG	AAATCGGCAAAATCCCTTTATAAATCAAAAGATAGCCCGAGATACGGTGTAGTGTGT	483
Db	5866	CG	AAATCGGCAAAATCCCTTTATAAATCAAAAGATAGCCCGAGATAGGGTTGTAGTGTGT	5807
QY	484	TCC	AGTTTGGAAACAAGAGTCACATTTAAAGACGTGGACTCCAACTCAAGGGCGAAA	543
Db	5806	TCC	AGTTTGGAAACAAGAGTCACATTTAAAGACGTGGACTCCAACTCAAGGGCGAAA	5747
QY	544	AAC	CGTCTATCAGGGCGGATGGCCCACTACGTGAACCATCATCCCAAAATCAAGTTTGGG	603
Db	5746	AAC	CGTCTATCAGGGCGGATGGCCCACTACGTGAACCATCATCCCAAAATCAAGTTTGGG	5687
QY	604	GT	CAGGTGCGGTAAAGCACTAATTCGGAACCTTAAGGGAGGCCCGCGATTTAGAGCTTG	663
Db	5686	GT	CAGGTGCGGTAAAGCACTAATTCGGAACCTTAAGGGAGGCCCGCGATTTAGAGCTTG	5627
QY	664	AC	GCGGAAGCCGGCAACCTGGCGAGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG	723
Db	5626	AC	GCGGAAGCCGGCAACCTGGCGAGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG	5567
QY	724	TAG	GGCGCTGGCAAGTGTACCGGTACAGCTGCGCGTAAACCAACACCCGCCGCTTAA	783
Db	5566	TAG	GGCGCTGGCAAGTGTACCGGTACAGCTGCGCGTAAACCAACACCCGCCGCTTAA	5507

RESULT	8	
ID	AAQ66630/c	
XX	AAQ66630 standard; DNA; 7294 BP.	
XX		
XX	AAQ66630;	
XX		
DT	23-JAN-1995 (first entry)	
XX		
DE	Right-half vector M131x421.	
XX		
XX	vector M131x421; right-half vector; randomised oligonucleotides;	
XX	surface expression; random peptide; constrained secondary structure;	
XX	pseudo wild-type M13 gene VIII; ds.	
XX	Synthetic.	
XX		
XX	W09411496-A.	
XX		
XX	26-MAY-1994.	
XX		
XX	09-NOV-1993; 93WO-US10850.	
XX		
XX	10-NOV-1992; 92US-0978893.	
XX		
XX	(IXSY-) IXSYS INC.	

CC elements and to gVIII. These vectors encode a pseudo-wild type gVIII product. This gene encodes the wild-type M13 gVIII amino acid sequence but has been changed at the nucleotide level to reduce homologous recombination with the wild-type gVIII contained on these vectors. The wild-type gVIII is present to ensure that at least some functional, non-fusion coat protein is produced. They also contain the expression elements for the peptide fusion proteins. A ribosome binding site and LacZ promoter/operator elements are present for transcription and translation of the peptide fusion proteins. Various restriction sites are present for the cloning of random peptides.

XX
SQ Sequence 7294 BP; 1796 A; 1527 C; 1553 G; 2418 T; 0 other;

Query Match 94.3%; Score 1147.6; DB 13; Length 7294;
Best Local Similarity 99.7%; Pred. No. 8.8e-208;
Matches 1150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 784 TGCAGGCTACAGGCGGCTACTAGTTCCTTTCAGAGCAGCTATAACGTCGTTTCCT 843
DB 5506 TGCAGGCTACAGGCGGCTACTAGTTCCTTTCAGAGCAGCTATAACGTCGTTTCCT 5447
QY 844 CGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTCAGACAGGAACG 903
DB 5446 CGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTCAGACAGGAACG 5387
QY 904 GTACGCCAGAAATCTTGAGAAAGTTCCTTTCAGAGCAGCTATAACGTCGTTTCCT 963
DB 5386 GTACGCCAGAAATCTTGAGAAAGTTCCTTTCAGAGCAGCTATAACGTCGTTTCCT 5327
QY 964 GTCCATACAGCAAAATTAACCGTTGAGCAATACCTTTCAGAGCAGCTATAACGTCGTTTCCT 1023
DB 5326 GTCCATACAGCAAAATTAACCGTTGAGCAATACCTTTCAGAGCAGCTATAACGTCGTTTCCT 5267
QY 1024 CCGTGTAGAGAACTCAAACTATCGGCTTCGTCGTTTCAGAGCAGCTATAACGTCGTTTCCT 1083
DB 5266 CCGTGTAGAGAACTCAAACTATCGGCTTCGTCGTTTCAGAGCAGCTATAACGTCGTTTCCT 5207
QY 1084 CAGCCATTCACAGAGAAACGCTCATGGAATACCTTTCAGAGCAGCTATAACGTCGTTTCCT 1143
DB 5206 CAGCCATTCACAGAGAAACGCTCATGGAATACCTTTCAGAGCAGCTATAACGTCGTTTCCT 5147
QY 1144 GAAATGGAATTTTACATTTGGCAGATTTCACAGTTCACAGCAGCTATAACGTCGTTTCCT 1203
DB 5146 GAAATGGAATTTTACATTTGGCAGATTTCACAGTTCACAGCAGCTATAACGTCGTTTCCT 5087
QY 1204 TCTGGCCACAGAG 1217
DB 5086 TCTGGCCACAGAG 5073

RESULT 9
AAQ24174/c
ID AAQ24174 standard; DNA; 7294 BP.

XX AAQ24174;
XX 19-JAN-1993 (first entry)
XX M13X421.
XX M13; cloning vectors; gVIII; pseudo-wild type; coat protein; RBS;
XX LacZ; ss.
XX Synthetic.
XX WO9206176-A.
XX 16-APR-1992.
XX 27-SEP-1991; 91WO-US07141.
XX 28-SEP-1990; 90US-0590664.
XX (IXSY-) IXSYS INC.
XX Huse WD;
XX WPI; 1992-150863/18.
XX Surface expression libraries of randomised peptide(s) -
XX comprising vectors contg. diverse populations of
XX oligonucleotide(s) having desirable bias of random codon
XX sequences
XX Disclosure; Page 85-88; 142pp; English.
XX The sequences given in AAQ24173-5 are vectors which allow the expression
XX of random peptides on the surface of M13. The vectors are produced by
XX combining separate vectors into a single larger vector. This system
XX produces random oligonucleotides functionally linked to expression

CC elements and to gVIII. These vectors encode a pseudo-wild type gVIII product. This gene encodes the wild-type M13 gVIII amino acid sequence but has been changed at the nucleotide level to reduce homologous recombination with the wild-type gVIII contained on these vectors. The wild-type gVIII is present to ensure that at least some functional, non-fusion coat protein is produced. They also contain the expression elements for the peptide fusion proteins. A ribosome binding site and LacZ promoter/operator elements are present for transcription and translation of the peptide fusion proteins. Various restriction sites are present for the cloning of random peptides.

XX
SQ Sequence 7294 BP; 1796 A; 1527 C; 1553 G; 2418 T; 0 other;

Query Match 94.3%; Score 1147.6; DB 13; Length 7294;
Best Local Similarity 99.7%; Pred. No. 8.8e-208;
Matches 1150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 64 ATCATGTTCATAGCTGTTTCCTGTTGAAATTTTATCCGCTCACAATTCACACACAT 123
DB 6226 ATCTGTCATAGCTGTTTCCTGTTGAAATTTTATCCGCTCACAATTCACACACAT 6167
QY 124 ACGAGCGGAGAGCATAAAGTGTAAAGCTGGGTCCCTTAATGAGTGAGCTAACTCACAATT 183
DB 6166 ACGAGCGGAGAGCATAAAGTGTAAAGCTGGGTCCCTTAATGAGTGAGCTAACTCACAATT 6107
QY 184 AATTCGCTTTCGCTCAGCTGCGGCTTTCAGTTCGGAACCTGTCGCCAGCTCATTA 243
DB 6106 AATTCGCTTTCGCTCAGCTGCGGCTTTCAGTTCGGAACCTGTCGCCAGCTCATTA 6047
QY 244 ATGAATTCGCGCAACGCGGGAGAGCGGTTTGGTATTTGGCGCCAGGTTTTC 303
DB 6046 ATGAATTCGCGCAACGCGGGAGAGCGGTTTGGTATTTGGCGCCAGGTTTTC 5987
QY 304 TTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCTTTCAGCCCTGCGCCCTGAGAGATT 363
DB 5986 TTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCTTTCAGCCCTGCGCCCTGAGAGATT 5927
QY 364 GCAGCAAGCGGCTCCAGCTGTTTGGCCAGAGCGGAAATTCCTTTGATGTTGTTTC 423
DB 5926 GCAGCAAGCGGCTCCAGCTGTTTGGCCAGAGCGGAAATTCCTTTGATGTTGTTTC 5867
QY 424 CGAAATTCGCAAAATCCCTTATTAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 483
DB 5866 CGAAATTCGCAAAATCCCTTATTAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGACAAGAGTCCACTATTAAGAGACGTGGGACTCCAACTCAAGAGGCGAAA 543
DB 5806 TCCAGTTTGGACAAGAGTCCACTATTAAGAGACGTGGGACTCCAACTCAAGAGGCGAAA 5747
QY 544 AACCGTCTATCAGGCGGATGCGCCACTGAGCTGAGCAATACCCCAATCAAGTTTTCGG 603
DB 5746 AACCGTCTATCAGGCGGATGCGCCACTGAGCTGAGCAATACCCCAATCAAGTTTTCGG 5687
QY 604 GTCCAGGTGCGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTGAGCGTTG 663
DB 5686 GTCCAGGTGCGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTGAGCGTTG 5627
QY 664 ACGGGGAAAGCGCGGAGAGCTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
DB 5626 ACGGGGAAAGCGCGGAGAGCTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5567
QY 724 TAGGGCGCTGCAAGTGTAGCGGTTCAGCTGCGGTAAACCAACACCCCGCGCTTAA 783
DB 5566 TAGGGCGCTGCGTGTAGTGTAGCGGTTCAGCTGCGGTAAACCAACACCCCGCGCTTAA 5507
QY 784 TGCAGCGCTACAGGCGCGTACTATGTTGTTTTCAGAGCAGCTATACGTCGTTTCCT 843
DB 5506 TGCAGCGCTACAGGCGCGTACTATGTTGTTTTCAGAGCAGCTATACGTCGTTTCCT 5447
QY 844 CTTTCGATCAGAGCGGAGCTTAAACAGAGCGGCTTAAAGGAGTTTTCAGACAGGAACG 903
DB 5446 CTTTCGATCAGAGCGGAGCTTAAACAGAGCGGCTTAAAGGAGTTTTCAGACAGGAACG 5387

QY 904 GTAGCCAGAAATCTTGAGAGTGTCTTTTATATCAGTCAGGCGCCAGTAAAGAGTCT 963
 Db 5386 GTAGCCAGAAATCTTGAGAGTGTCTTTTATATCAGTCAGGCGCCAGTAAAGAGTCT 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTTTTGTAGTAAATACATCATTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTTTTGTAGTAAATACATCATTG 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGTAATATCCAGACATATACCGC 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGTAATATCCAGACATATACCGC 5207
 QY 1084 CAGCCATTGCAACAGGAAACGCTCATGGAATPACCTACATTTTGCCTCAATCGTCT 1143
 Db 5206 CAGCCATTGCAACAGGAAACGCTCATGGAATPACCTACATTTTGCCTCAATCGTCT 5147
 QY 1144 GAAATGGATTATTTACATTTGGCAGATTTCCAGCTCACACGACGATTAATAAGGGACAT 1203
 Db 5146 GAAATGGATTATTTACATTTGGCAGATTTCCAGCTCACACGACGATTAATAAGGGACAT 5087
 QY 1204 TCTGGCCACACAGAG 1217
 Db 5086 TCTGGCCACACAGAG 5073

RESULT 10

AAQ24170/c

ID AAQ24170 standard; DNA; 7294 BP.

XX

AC AAQ24170;

XX

DT 19-JAN-1993 (first entry)

XX

DE M13IX42.

XX

KW M13; cloning vectors; gVIII; M13IX22; M13IX30; pseudo-wild type;

XX

KW coat protein; RBS; ss.

XX

OS Synthetic.

XX

FN W09206176-A.

XX

PD 16-APR-1992.

XX

XX 27-SEP-1991; 91WO-US07141.

XX

XX 28-SEP-1990; 90US-0590664.

XX

PA (IXSY-) IXSYS INC.

XX

PI Huse WD;

XX

DR WPI; 1992-150863/18.

XX

PT Surface expression libraries of randomised peptide(s) -
 PT comprising vectors contg. diverse populations of
 PT oligonucleotide(s) having desirable bias of random codon
 PT sequences

XX

PS Disclosure; Fig 5; 142pp; English.

XX

CC The sequences given in AAQ24170-2 are vectors which allow the
 CC expression of random peptides on the surface of M13. The vectors
 CC are produced by combining separate vectors into a single larger
 CC vector. This system produces random oligonucleotides functionally
 CC linked to expression elements and to gVIII. M13IX42 is used for
 CC sense strand oligonucleotide portions. It encodes a pseudo-wild type
 CC gVIII product. This gene encodes the wild-type M13 gVIII amino acid
 CC sequence but has been changed at the nucleotide level to reduce
 CC homologous recombination with the wild-type gVIII contained on the
 CC same vector. The wild-type gVIII is present to ensure that at least
 CC some functional, non-fusion coat protein is produced. M13IX22 is used

CC for anti-sense strand oligonucleotide portions. It contains the
 CC expression elements for the peptide fusion proteins. A ribosome
 CC binding site and LacZ promoter/operator elements are present for
 CC transcription and translation of the peptide fusion proteins. M13IX30
 CC contains a wild-type and pseudo-wild-type gVIII genes and various
 CC restriction sites for cloning of random peptides.

XX
 SQ Sequence 7294 BP; 1789 A; 1525 C; 1554 G; 2426 T; 0 other;

Query Match 94.0%; Score 1144.4; DB 13; Length 7294;
 Best Local Similarity 99.5%; Pred. No. 3.5e-207;
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 64 ATCATGTGTATAGCTGTTTCTCTGTGTAATTTGTTATCCGCTCACAAATTTCCACACAACT 123
 Db 6226 ATCTGTGTATAGCTGTTTCTCTGTGTAATTTGTTATCCGCTCACAAATTTCCACACAACT 6167
 QY 124 ACAGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAAGTGTAGTGAAGTGAAGTGAAGT 183
 Db 6166 ACAGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAAGTGTAGTGAAGTGAAGTGAAGT 6107
 QY 184 AATTGCGTTTGGCTCTCACTGCCCCCTTTCCAGTCGGGAACCTGCTGCCAGCTGCATTA 243
 Db 6106 AATTGCGTTTGGCTCTCACTGCCCCCTTTCCAGTCGGGAACCTGCTGCCAGCTGCATTA 6047
 QY 244 ATGNAATCGGCAACGCGGCGGAGAGGGGTTTCCGTATTGGGCCCGCAGGGTGGTTTTTC 303
 Db 6046 ATGNAATCGGCAACGCGGCGGAGAGGGGTTTCCGTATTGGGCCCGCAGGGTGGTTTTTC 5987
 QY 304 TTTTACACAGTGTAGACGGGCAACAGCTGATTTGCCCTTTCACCGCTGGCCCTGAGAGAGTT 363
 Db 5986 TTTTACACAGTGTAGACGGGCAACAGCTGATTTGCCCTTTCACCGCTGGCCCTGAGAGAGTT 5927
 QY 364 GCAGCAAGCGGTCACGCTGTTTGGCCCGAGCGGCAAAATCTGTTGATGTGGTTTC 423
 Db 5926 GCAGCAAGCGGTCACGCTGTTTGGCCCGAGCGGCAAAATCTGTTGATGTGGTTTC 5867
 QY 424 CGAAATCGGCAAAATCCCTTATTAATCAAAAGATATGCCCGAGATAGGTTGATGTGT 483
 Db 5866 CGAAATCGGCAAAATCCCTTATTAATCAAAAGATATGCCCGAGATAGGTTGATGTGT 5807
 QY 484 TCCAGTTTGAACAAAGAGTCCACTATTAAAGAACGTTGGACTCCAACTGCAAAAGGCGGAAA 543
 Db 5806 TCCAGTTTGAACAAAGAGTCCACTATTAAAGAACGTTGGACTCCAACTGCAAAAGGCGGAAA 5747
 QY 544 AACCGTCTATAGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG 603
 Db 5746 AACCGTCTATAGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG 5687
 QY 604 GTCGAGTGCCGTAAGCACTAAATCGGAACCTTAAGGAGCGCCCGGATTTAGAGCTTG 663
 Db 5686 TCGGAGTGCCGTAAGCACTAAATCGGAACCTTAAGGAGCGCCCGGATTTAGAGCTTG 5627
 QY 664 ACGGGGAAGCGCGGAGCGGCGGAGAAAGGAAAGGAAAGGAAAGGAGGCGCGC 723
 Db 5626 ACGGGGAAGCGCGGAGCGGCGGAGAAAGGAAAGGAAAGGAAAGGAGGCGCGC 5567
 QY 724 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGCTAACCCACACACCGCCCGCGCTTAA 783
 Db 5566 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGCTAACCCACACACCGCCCGCGCTTAA 5507
 QY 784 TGGCCCGCTACAGGCGCGTACTATGTTGCTTTTCCAGGACGATATACGTCGTTTCT 843
 Db 5506 TGGCCCGCTACAGGCGCGTACTATGTTGCTTTTCCAGGACGATATACGTCGTTTCT 5447
 QY 844 CGTTTGAATCAGAGCGGAGCTAAACAGGAGCGGCTTTAAAGGGATTTTAGACGAACG 903
 Db 5446 CGTTTGAATCAGAGCGGAGCTAAACAGGAGCGGCTTTAAAGGGATTTTAGACGAACG 5387
 QY 904 GTAGCCAGAAATCTTGAGAGTGTCTTTTATATCAGTCAGGCGCCAGTAAAGAGTCT 963
 Db 5386 GTAGCCAGAAATCTTGAGAGTGTCTTTTATATCAGTCAGGCGCCAGTAAAGAGTCT 5327

CC exemplification of the present invention.

QY 964 GTCCATCAGCAATTAACCGTTGTAGCAATACCTTTTGTAGTAATAACATCACTTG 1023
 XX
 SQ
 Sequence 7300 BP; 1789 A; 1565 C; 1539 G; 2407 T; 0 other;
 Query Match 93.8%; Score 1141; DB 22; Length 7300;
 Best Local Similarity 96.6%; Pred. No. 1.5e-206;
 Matches 1176; Conservative 0; Mismatches 40; Indels 1; Gaps 1;
 QY 1 GCCAAGCTTGCATCCCTGCGAGTGCAGCTTAGAGGATCCCGGGTACCGAGCTCAATTC 60
 DB 6390 GCCAAGCTTGCATCCCTGCGAGTGCAGCTTAGAGGATCCCGGGTACCGAGCTCAATTC 6331
 QY 61 GTAATCATGTCTAGCTGTTTCTGTGTGTAATTTTATCCGTCAAAATTCACACAA 120
 DB 6330 GTAATCATGTCTAGCTGTTTCTGTGTGTAATTTTATCCGTCAAAATTCACACAA 6271
 QY 121 CATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTGCCTAATGAGTGAAGTCACTCAC 180
 DB 6270 CATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTGCCTAATGAGTGAAGTCACTCAC 6211
 QY 181 ATTAATTTGCTTGGCTGCTCACTGCCCGCTTTCCAGTCCGGAACCTGTCTGCCAGCTGCA 240
 DB 6210 ATTAATTTGCTTGGCTGCTCACTGCCCGCTTTCCAGTCCGGAACCTGTCTGCCAGCTGCA 6151
 QY 241 TTAATGAATCGGCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCGCCAGGGTGGTTT 300
 DB 6150 TTAATGAATCGGCAACCGCGGGGAGAGCGGTTTGGCTATTGGGCGCCAGGGTGGTTT 6091
 QY 301 TTCTTTTACCAGTGAAGCGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGA 360
 DB 6090 TTCTTTTACCAGTGAAGCGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGA 6031
 QY 361 GTTCAGCAAGCGTCCAGCTGTTTCCCGCAGCAGCGGAAATCTCTTTGATGGTGG 420
 DB 6030 GTTCAGCAAGCGTCCAGCTGTTTCCCGCAGCAGCGGAAATCTCTTTGATGGTGG 5971
 QY 421 TTCCGAAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT 480
 DB 5970 TTCCGAAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT 5911
 QY 481 TGTTCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCAACGTCAGAGGGGG 540
 DB 5910 TGTTCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCAACGTCAGAGGGGG 5851
 QY 541 AAAAACCGTCTATCAGGGCGATGGCCCTTACGTGAACCATCACCCAAATCAAGTGTGT 600
 DB 5850 AAAAACCGTCTATCAGGGCGATGGCCCTTACGTGAACCATCACCCAAATCAAGTGTGT 5791
 QY 601 GGGGTCGAGGTCGGTAAAGCACTAAATCGGAACCTTAAGGAGGAGCCCGATTTAGAGC 660
 DB 5790 GGGGTCGAGGTCGGTAAAGCACTAAATCGGAACCTTAAGGAGGAGCCCGATTTAGAGC 5731
 QY 661 TTTGAGGGGAAAGCCGCGCAACGTTGGCGAAGAAAGGAGGAAAGGAGAGCGGG 720
 DB 5730 TTTGAGGGGAAAGCCGCGCAACGTTGGCGAAGAAAGGAGGAAAGGAGAGCGGG 5671
 QY 721 CGCTAGGGCGCTGGCAAGTGTACGGTCAAGCTGAGGAGGAGCCCGATTTAGAGC 780
 DB 5670 CGCTAGGGCGCTGGCAAGTGTACGGTCAAGCTGAGGAGGAGCCCGATTTAGAGC 5611
 QY 781 TAATGCGCGCTACAGGGCGCGTACTATGTTGTTGAGGAGCAGCTATAACGTCGTTT 840
 DB 5610 TAATGCGCGCTACAGGGCGCGTACTATGTTGTTGAGGAGCAGCTATAACGTCGTTT 5551
 QY 841 CCTCGTTGGAATCAGAGCGGAGCTAAACAGGAGGCGGATTTAAAGGATTTTACAGAGGA 900
 DB 5550 CCTCGTTGGAATCAGAGCGGAGCTAAACAGGAGGCGGATTTAAAGGATTTTACAGAGGA 5491
 QY 901 ACGGTACGCGAGCAATCTTTGACAGAGTGTATTAATCAGTGAAGCCAGGAGTAAAGAG 960
 DB 5490 ACGGTACGCGAGCAATCTTTGACAGAGTGTATTAATCAGTGAAGCCAGGAGTAAAGAG 5431

RESULT 11

AAF59234/c
 ID AAF59234 standard; DNA: 7300 BP.

XX AAF59234;

XX 26-APR-2001 (first entry)

XX M13mp18 nucleotide sequence.

XX M13mp18; living organism; dead organism; nucleic acid copying;
 isostatic condition; temperature; buffer; ionic strength; ds.

XX Bacteriophage M13.

XX US2001000077-A1.

XX 29-MAR-2001.

XX 30-NOV-2000; 2000US-0727349.

XX 03-FEB-1998; 98US-0302818.

XX (ENGELHARDT D L.

XX (STAVR/ STAVRIANOPOULOS J G.

XX (RABB/ RABBANI E.

XX (DONE/ DONEGAN J J.

XX Engelhardt DL, Stavrianopoulos JG, Rabbani E, Donegan JJ;

XX WPI; 2001-202468/20.

XX Producing copies of specific nucleic acids in vitro, without the need
 of intermediate structures, useful for determining if samples have come
 from living or dead organisms -

XX Disclosure; Fig 5: 4lpp; English.

XX The present invention describes a method for producing, in vitro, copies
 of a specific nucleic acid. The process does not require the use of
 intermediate structures for the production of the nucleic acid. The
 method comprises: (a) providing a nucleic acid sample containing the
 specific sequence; (b) contacting the sample with a mixture containing:
 (i) nucleic acid precursors; (ii) specific nucleic acid primers, each
 complementary to a distinct region of the sequence; and (iii) a nucleic
 acid producing catalyst; and (c) allowing the mixture to react under
 isostatic conditions of temperature, buffer and ionic strength. The
 method can be used for producing copies of specific nucleic acids in
 vitro. The process can be used to determine if a specific target
 nucleic acid was derived from a living or deceased organism. The present
 sequence represents a M13mp18 nucleotide sequence which is given in the

QY 961 TCTGTCATCAGCAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAGTAATAACATCAC 1020
 Db 5430 TCTGTCATCAGCAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAGTAATAACATCAC 5371
 QY 1021 TTGCCTGAGTAGAAGCACTCAAACTATCGGCTTGTGTAATATCCAGAACATATTAC 1080
 Db 5370 TTGCCTGAGTAG-AGAAGTCAAACTATCGGCTTGTGTAATATCCAGAACATATTAC 5312
 QY 1081 CGCCAGCCATTTGACAGGAGAAACGCTCATGGAATACCTACATTTTTCAGCGCTCAATCG 1140
 Db 5311 CGCCAGCCATTTGACAGGAGAAACGCTCATGGAATACCTACATTTTTCAGCGCTCAATCG 5252
 QY 1141 TCTGAAATGGATTATTACATTTGGCAGATTCACCACTCAGCAGCAGCAATTAATAAGGGA 1200
 Db 5251 CGTAGATACCTGGCAGACAGCAATATTTTGAATGGCTATTAGTCTTTAATAAAGGGA 5192
 QY 1201 CATTCGGCCACAGAG 1217
 Db 5191 CATTCGGCCACAGAG 5175

RESULT 12
 AA251028/C
 ID AA251028 standard; DNA; 7084 BP.
 XX
 AC
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Modified filamentous phage.
 XX
 KW Modified filamentous phage; polypeptide display; expression vector;
 KW major coat protein; MCP; ligand-binding heterodimeric antibody; ligand;
 KW ss.
 XX Bacteriophage.
 OS
 XX W0200009715-A1.
 PN
 XX
 PD 24-FEB-2000.
 XX
 PF 11-AUG-1999; 99WO-US18207.
 XX
 PR 12-AUG-1998; 98US-0096326.
 PR 24-DEC-1998; 98US-0198839.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Kang AS;
 XX
 DR WPI; 2000-224350/19.
 XX
 PT New modified filamentous phage vectors, useful for the phage display of
 XX polypeptides -
 PS Disclosure; Fig 4; 38pp; English.
 XX

CC The present sequence is a modified filamentous phage used for modulation
 CC of polypeptide display on the surface which permits facile manipulation
 CC of the valency of display. The gene encoding the polypeptide is fused
 CC into a synthetic copy of a major coat protein (MCP) which enables
 CC incorporation into the phage during assembly of the filament. Modified
 CC filamentous phage expression vector includes a wild type MCP gene; a
 CC leaky inducible promoter; a synthetic MCP gene; and a directional
 CC cloning site for receiving a nucleotide insert. The vectors can be used
 CC for the expression of polypeptides such as ligand-binding heterodimeric
 CC antibodies. They can be used for identifying ligands and for
 CC characterising antibodies.

SQ Sequence 7084 BP; 1739 A; 1469 C; 1485 G; 2391 T; 0 other;
 Query Match 93.7%; Score 1140.4; DB 21; Length 7084;

Best Local Similarity 99.9%; Pred. No. 2e-206;
 Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 GCTGTTTCCGTGTGAAATTTGTTATCCGCTCACAATTCACACAATACAGCGCGAAG 135
 Db 7084 GCTGTTTCCGTGTGAAATTTGTTATCCGCTCACAATTCACACAATACAGCGCGAAG 7025
 QY 136 CATAAAGTGTAAAGCCCTGGGCTGCTAATGAGTGAGCTAACTCAATTAATGCGTTGCG 195
 Db 7024 CATAAAGTGTAAAGCCCTGGGCTGCTAATGAGTGAGCTAACTCAATTAATGCGTTGCG 6965
 QY 196 CTCACTCCCGCTTTCAGTTCGGGAAACCTGCTGCGCAGCTGCAATTAATGAATCGGCA 255
 Db 6964 CTCACTCCCGCTTTCAGTTCGGGAAACCTGCTGCGCAGCTGCAATTAATGAATCGGCA 6905
 QY 256 ACAGCGGGGAGAGCGGTTTGGCTATTGGGCGCCAGGTTGGTTTCTTTTCCACCACTG 315
 Db 6904 ACAGCGGGGAGAGCGGTTTGGCTATTGGGCGCCAGGTTGGTTTCTTTTCCACCACTG 6845
 QY 316 AGACGGCAACAGCTGATTCGCCCTTTCACCGCTGGCCCTGAGAGAGTTGACGAAGCGGT 375
 Db 6844 AGACGGCAACAGCTGATTCGCCCTTTCACCGCTGGCCCTGAGAGAGTTGACGAAGCGGT 6785
 QY 376 CCACGCTGTTTTCGCCCGCAGCAGCGGAAATCCTGTTTGTGATGGTTCGAAATCGCAA 435
 Db 6784 CCACGCTGTTTTCGCCCGCAGCAGCGGAAATCCTGTTTGTGATGGTTCGAAATCGCAA 6725
 QY 436 AATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGTGTTCCACCTTTGGAA 495
 Db 6724 AATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGTGTTCCACCTTTGGAA 6665
 QY 496 CAAGAGTCCACTATTAAAGAACGTGACCTCAACGTCAGAGGCGGAAACCTCTATCA 555
 Db 6664 CAAGAGTCCACTATTAAAGAACGTGACCTCAACGTCAGAGGCGGAAACCTCTATCA 6605
 QY 556 GGGCGATGCCCGCAGCTGTAACCCATCAATCAAGTTTGGGGTCGAGAGTGCCG 615
 Db 6604 GGGCGATGCCCGCAGCTGTAACCCATCAATCAAGTTTGGGGTCGAGAGTGCCG 6545
 QY 616 TAAAGCAGCTAAATCGAACCCCTAAAGGAGAGCCCGATTTAGAGCTTGACGGGAAAGCC 675
 Db 6544 TAAAGCAGCTAAATCGAACCCCTAAAGGAGAGCCCGATTTAGAGCTTGACGGGAAAGCC 6485
 QY 676 GCGAAGCTGCGGAGAAAGGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
 Db 6484 GCGAAGCTGCGGAGAAAGGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6425
 QY 736 AAGTGTAGCGTACGCTGCGGTAAACCAACACACCCCGCGCTTAATGCGCGCTACA 795
 Db 6424 AAGTGTAGCGTACGCTGCGGTAAACCAACACACCCCGCGCTTAATGCGCGCTACA 6365
 QY 796 GGGCGCGTACTATGTTGCTTTGACGAGCAGTATAACGTTCTTCTCGTTGGGAATCAG 855
 Db 6364 GGGCGCGTACTATGTTGCTTTGACGAGCAGTATAACGTTCTTCTCGTTGGGAATCAG 6305
 QY 856 AGCGGGAGCTAAACAGAGCGCGATTAAGGATTTTACAGAGAACGCTACGCCAGAT 915
 Db 6304 AGCGGGAGCTAAACAGAGCGCGATTAAGGATTTTACAGAGAACGCTACGCCAGAT 6245
 QY 916 CTTGAGAAGTGTGTTTATAATCAGTGAGCGCCAGGTAAGAGAGTCTGTCCATCACGA 975
 Db 6244 CTTGAGAAGTGTGTTTATAATCAGTGAGCGCCAGGTAAGAGAGTCTGTCCATCACGA 6185
 QY 976 AATTAAACGTTGTAGCAATCTTCTTTGATTAGTAATTAACATCACTTCCCTGAGTAGAG 1035
 Db 6184 AATTAAACGTTGTAGCAATCTTCTTTGATTAGTAATTAACATCACTTCCCTGAGTAGAG 6125
 QY 1036 AACTCAAACTATCGGCTTCTGCTGTAATATCCAGAACATATTACCGCCAGCCATTGCA 1095
 Db 6124 AACTCAAACTATCGGCTTCTGCTGTAATATCCAGAACATATTACCGCCAGCCATTGCA 6065
 QY 1096 CAGGAAACGCTCATGGAATACCTACATTTTCCAGCTCAATCGTCTGGAATGATTAT 1155

Db 6064 CAGGAAAAACGCTCATGGAAATACCTACATTTTGACGCTCAATCGTCTGAATGGATTAT 6005
QY 1156 TTACATTGGCAGATTACACAGTCCACAGCAGTAAATAAAGGACATTTCTGGCCAAACAG 1215
Db 6004 TTACATTGGCAGATTACACAGTCCACAGCAGTAAATAAAGGACATTTCTGGCCAAACAG 5945
QY 1216 AG 1217
Db 5944 AG 5943

RESULT 13
AAV03651/c
ID AAV03651 standard; DNA; 7317 BP.

XX AAV03651;
XX AC
XX 02-APR-1998 (first entry)
XX DE M13-based vector M13IX11.
XX Vector construction; T-cell receptor; antibody production; diagnosis;
KW heteromeric receptor; immunoglobulin superfamily; therapy; circular;
KW M13-based vector; ds.
XX Synthetic.
XX OS
XX US5698426-A.
XX PN 16-DEC-1997.
XX PD
XX 05-JUN-1995; 95US-0464136.
XX 27-SEP-1991; 91US-0767136.
XX 28-SEP-1990; 90US-0590219.
XX 13-SEP-1993; 93US-0120648.
XX 01-DEC-1984; 94US-0349131.
XX 03-JUN-1995; 95US-0464136.
XX (IXSY-) IXSYS INC.
XX Huse WD;
XX WPT; 1998-051489/05.
XX Construction of heteromeric receptor libraries - by combining
PT vectors encoding different immunoglobulin fragments

XX Example 1; Column 27-34; 57pp; English.
XX This sequence represents a M13-based vector constructed using the method
CC of the invention, and the primers shown in AAV03629-V03649. The method
CC of the invention is for constructing a diverse population of vectors
CC capable of expressing diverse populations of first and second
CC polypeptides which form a diverse population of heteromeric receptors of
CC the immunoglobulin superfamily, and comprises: (a) operationally linking
CC to a first vector a first population of diverse DNA sequences within a
CC first gene family encoding a diverse population of first polypeptides of
CC the heteromeric receptor of the immunoglobulin superfamily, the first
CC vector having two pairs of restriction sites symmetrically oriented about
CC a cloning site; (b) operationally linking to a second vector a second
CC population of diverse DNA sequences within a second gene family encoding
CC a diverse population of second polypeptides of the heteromeric receptor
CC of the immunoglobulin superfamily, the second vector having two pairs of
CC restriction sites symmetrically oriented about a cloning site in an
CC identical orientation to that of the first vector, where polypeptides
CC encoded by the first and second gene families are known to form
CC heteromeric receptors of the immunoglobulin superfamily; and (c)
CC combining the vector sequences produced by steps (a) and (b) under
CC conditions which allow only the operational combinations of the vector
CC sequences containing the first and second populations of diverse DNA
CC sequences. The method is used to produce diverse populations of
CC antibodies or T-cell receptors for diagnostic or therapeutic purposes.

XX SQ Sequence 7317 BP; 1787 A; 1555 C; 1547 G; 2428 T; 0 other;
Query Match 93.0%; Score 1131.4; DB 19; Length 7317;
Best Local Similarity 99.5%; Pred. NO. 1e-204;
Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 77 CTGTTTCCTGCTGAAATTTGTTATCCGCTCACAATTCACACAACATACGAGCGGAAGC 136
Db 6214 CTCTTTGGCGTGTGAATTTGTTATCCGCTCACAATTCACACAACATACGAGCGGAAGC 6155
QY 137 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGTAACTACATTAATTCGGTTGCC 196
Db 6154 ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGTAACTACATTAATTCGGTTGCC 6095
QY 197 TCATGCGCGCTTTCCAGTCCGGGAAACCTGTGTCGCCAGCTGCATTAATTCGGGCCAA 256
Db 6094 TCATGCGCGCTTTCCAGTCCGGGAAACCTGTGTCGCCAGCTGCATTAATTCGGGCCAA 6035
QY 257 CGCGGGGAGAGCGGTTTGGCTATTGGCGCCAGGTTGGTTTCTTTTCCACCACTGA 316
Db 6034 CGCGGGGAGAGCGGTTTGGCTATTGGCGCCAGGTTGGTTTCTTTTCCACCACTGA 5975
QY 317 GACGGCAACAGCTGATTGCCCTTCCACGCTGGCCCTGAGAGAGTTGACGAGCGGTC 376
Db 5974 GACGGCAACAGCTGATTGCCCTTCCACGCTGGCCCTGAGAGAGTTGACGAGCGGTC 5915
QY 377 CACGCTGTTTCCCGCAGCAGGGGAAAATCTGTTTGTAGTGGTTCGGAATTCGGCAAA 436
Db 5914 CACGCTGTTTCCCGCAGCAGGGGAAAATCTGTTTGTAGTGGTTCGGAATTCGGCAAA 5855
QY 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTGTTTCCAGTTTGAAC 496
Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTGTTTCCAGTTTGAAC 5795
QY 497 AAGAGTCCACTATTAAGAAACGTTGACTCCACGTCAAGGCGGGAAGAAACCGTCTATCAG 556
Db 5794 AAGAGTCCACTATTAAGAAACGTTGACTCCACGTCAAGGCGGGAAGAAACCGTCTATCAG 5735
QY 557 GCGGATGCGCCACTACGTGAAACCATCACCAATCAAGTTTGTGGGTTCGAGTGCCT 616
Db 5734 GCGGATGCGCCACTACGTGAAACCATCACCAATCAAGTTTGTGGGTTCGAGTGCCT 5675
QY 617 AAGCACTAAATCGGAACCTTAAAGGAGAGCCCGGATTTAGAGCTTGACGGGGAAGCCG 676
Db 5674 AAGCACTAAATCGGAACCTTAAAGGAGAGCCCGGATTTAGAGCTTGACGGGGAAGCCG 5615
QY 677 GCGAAGTGGCGAGAAAGGAGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 736
Db 5614 GCGAAGTGGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5555
QY 737 AGTGTAGCGGTACGCTGCGCGTAACACACACACACCGCCGCTTAATTCGCCGCTACAG 796
Db 5554 AGTGTAGCGGTACGCTGCGCGTAACACACACACACCGCCGCTTAATTCGCCGCTACAG 5495
QY 797 GCGCGTACTATGTTGCTTTTGTAGCAGCAGGTATTAACGTGCTTCTCTGTTGGAATCAGA 856
Db 5494 GCGCGTACTATGTTGCTTTTGTAGCAGCAGGTATTAACGTGCTTCTCTGTTGGAATCAGA 5435
QY 857 GCGGGAGCTAAACAGAGGAGCGGATTAAGGGATTTTACAGAGGAGGAGGAGGAGGAGGAG 916
Db 5434 GCGGGAGCTAAACAGAGGAGCGGATTAAGGGATTTTACAGAGGAGGAGGAGGAGGAGGAG 5375
QY 917 TTGAGAAGTGTGTTTATAATCAAGTGGCGCCAGGTAAGAGAGTCTCTCCATCACGCAA 976
Db 5374 TTGAGAAGTGTGTTTATAATCAAGTGGCGCCAGGTAAGAGAGTCTCTCCATCACGCAA 5315
QY 977 ATTAACCGTTGTAGCAATACCTTTTGTAGTATTAATCAATCACTTGTGCTGAGTGAAGA 1036
Db 5314 ATTAACCGTTGTAGCAATACCTTTTGTAGTATTAATCAATCACTTGTGCTGAGTGAAGA 5255
QY 1037 ACTCAACATATCGGCCCTTGGTGGTAAATTCACAGAACATATTTACCGCCAGCCATTGCAAC 1096

Db 5254 ACTCAAACTATCGGCTTGGTGTATATCCAGAAACAATATACCGCCAGCCATTGCAAC 5195
 Qy 1097 AGGAAAAACGCTCATGGAAATACCTTACATTTTGACGCTCAATCGTGAATGGATTATT 1156
 Db 5194 AGGAAAAACGCTCATGGAAATACCTTACATTTTGACGCTCAATCGTGAATGGATTATT 5135
 Qy 1157 TACATTTGGCAGATTCCACAGTCACACGACCAAGTAATAAAAGGAGCATTTCTGGCCCAACAGA 1216
 Db 5134 TACATTTGGCAGATTCCACAGTCACACGACCAAGTAATAAAAGGAGCATTTCTGGCCCAACAGA 5075
 Qy 1217 G 1217
 Db 5074 G 5074

RESULT 14
 AAX16953/c
 ID AAX16953 standard; DNA; 7317 BP.

AC AAX16953;

XX 11-MAY-1999 (first entry)

DE Plasmid M13IX11.

XX Heteromeric; receptor; immunoglobulin; superfamily; plasmid; primer; PCR;
 KW bacteriophage; fusion protein; amplification; heavy chain; light chain;
 KW Immune system; diagnosis; cyclic; circular; ds.

OS Synthetic.

XX US5871974-A.

XX 16-FEB-1999.

XX 02-DEC-1994; 94US-0349131.

XX 27-SEP-1991; 91US-0767136.

XX 28-SEP-1990; 90US-0590219.

XX 13-SEP-1993; 93US-0120548.

XX 02-DEC-1994; 94US-0349131.

XX (IXSY-) IXSVS INC.

XX Huse WD;

XX WPI; 1999-166647/14.

XX New surface expression libraries expressing heteromeric receptors -
 PT comprising cells containing vectors containing combinations of DNA
 PT sequences encoding first and second polypeptides

PS Example 1; Fig 3A-C; 58pp; English.

XX The invention relates to the expression of heteromeric receptor
 CC proteins, e.g. from an immunoglobulin (Ig) superfamily, in cells
 CC containing the heteromeric receptor genes on a single plasmid.
 CC Especially mentioned, the cell may be a bacteriophage, where the receptor
 CC protein are expressed as fusion proteins with the surface protein gpIII.
 CC This sequence represents the plasmid M13IX11 which is used for expression
 CC of the light chain proteins. The plasmid is constructed using primers
 CC AAX16938-X16952. The methods can be used to generate diverse populations
 CC of heteromeric receptors which mimic the natural immune system and can be
 CC used for diagnostic and therapeutic purposes.

XX Sequence 7317 BP; 1787 A; 1555 C; 1547 G; 2428 T; 0 other;

Query Match 93.0%; Score 1131.4; DB 20; Length 7317;
 Best Local Similarity 99.5%; Pred. No. 1e-204;
 Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 77 CTGCTTTCTGCTGTAATCTGTTATCCGCTCACAATTCACACACATACAGCGCGAAGC 136
 Db 6214 CTCTTTGGCGTGTGAATCTGTTATCCGCTCACAATTCACACACATACAGCGCGAAGC 6155
 Qy 137 ATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGCTAACTCACTAATTAATTTGCTTGGCG 196
 Db 6154 ATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGCTAACTCACTAATTAATTTGCTTGGCG 6095
 Qy 197 TCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGTCAGCTGCAATTAATGAATCGGCCAA 256
 Db 6094 TCACTGCCCGCTTTCCAGTCGGGAAACCTGCTGTCAGCTGCAATTAATGAATCGGCCAA 6035
 Qy 257 CGCGGGGAGAGGCGGTTTGGCTATTGGGCGCCAGGCTGTTTCTTTTCACCACTGA 316
 Db 6034 CGCGGGGAGAGGCGGTTTGGCTATTGGGCGCCAGGCTGTTTCTTTTCACCACTGA 5975
 Qy 317 GACGGGCAACAGCTGATTCCCTTCCAGCTGCGCTTGAGAGAGTTGCAAGCAAGCGGTC 376
 Db 5974 GACGGGCAACAGCTGATTCCCTTCCAGCTGCGCTTGAGAGAGTTGCAAGCAAGCGGTC 5915
 Qy 377 CACGCTGGTTTGGCCCGCAGCAGCGGAAATCTCTGTTGATGGTGGTTCGGAATCGGCAAA 436
 Db 5914 CACGCTGGTTTGGCCCGCAGCAGCGGAAATCTCTGTTGATGGTGGTTCGGAATCGGCAAA 5855
 Qy 437 ATCCCTTATAAATCAAAAGCAATAGCCCGCTGAGAGAGTTGCAAGCAAGCGGTC 496
 Db 5854 ATCCCTTATAAATCAAAAGCAATAGCCCGCTGAGAGAGTTGCAAGCAAGCGGTC 5795
 Qy 497 AAGAGTCCACTATTAAAGAACTGGACTCCAACGCTCAAGGGGCAAAACCGCTTATCAG 556
 Db 5794 AAGAGTCCACTATTAAAGAACTGGACTCCAACGCTCAAGGGGCAAAACCGCTTATCAG 5735
 Qy 557 GCGGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGGGTTCGAGGTCGCGT 616
 Db 5734 GCGGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGGGTTCGAGGTCGCGT 5675
 Qy 617 AAAGCACTAAATTCGGAACCCCTAAAGGGAGCCCGCTTAAAGAGCTTTAGAGCTTTAGCGGGGAAAGCCG 676
 Db 5674 AAAGCACTAAATTCGGAACCCCTAAAGGGAGCCCGCTTAAAGAGCTTTAGAGCTTTAGCGGGGAAAGCCG 5615
 Qy 677 GCGAACGTGGCGAGAAAGGAGGAAAGCAAGGAGCGGGGCGCTAGGGCGCTGGCA 736
 Db 5614 GCGAACGTGGCGAGAAAGGAGGAAAGCAAGGAGCGGGGCGCTAGGGCGCTGGCA 5555
 Qy 737 AGTGTAGCGGTACGCTGCGGTAAACCAACCCCGCTTAAAGAGCTTTAGAGCTTTAGCGGGGAAAGCCG 796
 Db 5554 AGTGTAGCGGTACGCTGCGGTAAACCAACCCCGCTTAAAGAGCTTTAGAGCTTTAGCGGGGAAAGCCG 5495
 Qy 797 GCGCGTACTATGTTGCTTTGACGAGCAGCTATTAACGTTCTCTCTGTTGGAATCAGA 856
 Db 5494 GCGCGTACTATGTTGCTTTGACGAGCAGCTATTAACGTTCTCTCTGTTGGAATCAGA 5435
 Qy 857 GCGGAGCTAAACAGGAGGCGGATTAAAGGGATTTTACAGGAGCAAGCGGTACGCCAGAATC 916
 Db 5434 GCGGAGCTAAACAGGAGGCGGATTAAAGGGATTTTACAGGAGCAAGCGGTACGCCAGAATC 5375
 Qy 917 TTGAGAAGTGTTTTATAATCAGTGAGGCGCCAGGAGTAAAGAGCTGTCTCCATCACGCAA 976
 Db 5374 TTGAGAAGTGTTTTATAATCAGTGAGGCGCCAGGAGTAAAGAGCTGTCTCCATCACGCAA 5315
 Qy 977 ATTAACCGTTGTAGCAATACATCTTTGATTAATTAACATCATCTGCTGAGTAGAAGA 1036
 Db 5314 ATTAACCGTTGTAGCAATACATCTTTGATTAATTAACATCATCTGCTGAGTAGAAGA 5255
 Qy 1037 ACTCAAACTATCGGCTTGGCTGTTAAATCCAGAACATATACCGCCAGCCATTCGCAAC 1096
 Db 5254 ACTCAAACTATCGGCTTGGCTGTTAAATCCAGAACATATACCGCCAGCCATTCGCAAC 5195
 Qy 1097 AGGAAAAACGCTCATGGAAATACCTTACATTTTGACGCTCAATCTGCTCTGAAATGGATTATT 1156
 Db 5194 AGGAAAAACGCTCATGGAAATACCTTACATTTTGACGCTCAATCTGCTCTGAAATGGATTATT 5135
 Qy 1157 TACATTTGGCAGATTCCACAGTCACACGACCAAGTAATAAAAGGAGCATTTCTGGCCCAACAGA 1216

[illegible]1217 G 1217
Ov

5074 G 5074

RESULT 15

AAZ91525/C
DNA: 7317 BP.

AAZ91525/C
ID 22701525 standard: DNA: 7317 bp.

XX
APPROPRIATE.XX
DE 35-MAY-2000 (first entry)[illegible]

XX = heteromeric receptor; prokaryotic cell: heteromeric receptor;

KW Bacteriophage M13 vector; prokaryotic cell; heteromeric icosahedral virus; filamentous bacteriophage: cloning;

KW antibody; immune system; ds

XX

OS Mus sp.

OS Bacteriophages

XX

PN US6027933-A.

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1000-0000-0000-0000

PD 22-FEB-2000.

XX
05 JUN 1995 05JIS-0470297.

05-JUN-1995; 9303-04/0237;

XX
PP 01-DEC-1994: 94US-0349131.

PR	01-DEC-1994,	510
PR	27-SEP-1991;	91US

PR 28-SEP-1990;
PR 28-SEP-1990;

13-SEP-1993; 93US-0

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PA (IXSY-) IXSYS INC.

XX
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PI Huse WD;
XX
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DR WPI; 2000-194835/17.
XX
XX Kit for the preparation of vectors for the coexpression of two or more
PT DNA sequences encoding proteins that form heteromeric receptors -
XX
XX
XX Example 1; Fig 3; 58pp; English.
PS

Example 47. A291529. *See Example 46.*

The present invention describes a kit (I) for the preparation of vectors for the coexpression of two or more DNA sequences encoding polypeptides comprising two vectors which operatively combine through two pairs of restriction sites to form a single vector. The kit is useful for the preparation of vectors for the coexpression of two or more DNA sequences encoding polypeptides which from heteromeric receptors. The kit simply and efficiently generates a large repertoire of diverse combinations of heteromeric receptors. Only proper combinations of vector portions are randomly brought together for the coexpression of different DNA sequences without loss of population size or diversity. AAZ91524 to AAZ91528 represent bacteriophage M13 vector nucleotide sequences constructed in the exemplification of the present invention. AAZ91529 to AAZ91599 represent oligonucleotides used in the construction of vectors for the exemplification of the present invention.

XX
= 3317 3317 1797 1. 1555 C. 1547 G: 2428 T: 0 other;

SQ Sequence 7317 BP; 178/ A; 1533 C; 1547 G; 2420 T; 3080 T

[illegible]

Db 6214 CTCCTTGGCGTGGAATGTTATCCGCTCACAAATCCACACAACATACGAGCCGGAGC 0155

Thu Aug 1 12:08:39 2002

us-10-014-743-1.rng

Page 16

QY 1217 G 1217
Db 5074 G 5074

Search completed: August 1, 2002, 09:37:26
Job time: 6762 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:40:39 : Search time 87.24 Seconds
(without alignments)
3426.593 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAAGCTTCATCCCTGCA.....GGACATTCGCCACACAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_NA:*
- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1217	100.0	1217	1	US-08-726-462B-1	Sequence 1, Appli
2	1217	100.0	1217	2	US-08-642-330-1	Sequence 1, Appli
3	1217	100.0	1217	2	US-09-046-203-1	Sequence 1, Appli
4	1217	100.0	1217	3	US-09-272-104-1	Sequence 1, Appli
5	1217	100.0	1217	4	US-09-272-097-1	Sequence 1, Appli
6	1150.8	94.6	7294	1	US-08-440-787A-1	Sequence 5, Appli
7	1150.8	94.6	7294	1	US-08-440-787A-5	Sequence 1, Appli
8	1150.8	94.6	7294	4	US-08-367-685-1	Sequence 1, Appli
9	1150.8	94.6	7294	4	US-08-367-685-5	Sequence 5, Appli
10	1150.8	94.6	7294	5	PCT-US91-07141-1	Sequence 1, Appli
11	1150.8	94.6	7294	5	PCT-US91-07141-5	Sequence 5, Appli
12	1140.4	93.7	7083	4	US-09-198-839-1	Sequence 1, Appli
13	1131.4	93.0	7317	4	US-08-464-136-2	Sequence 2, Appli
14	1131.4	93.0	7317	2	US-08-349-131-2	Sequence 2, Appli
15	1131.4	93.0	7317	3	US-08-470-297A-2	Sequence 2, Appli
16	1131.4	93.0	7317	5	PCT-US91-07149-2	Sequence 2, Appli
17	1131.4	93.0	7320	1	US-08-440-787A-2	Sequence 2, Appli
18	1131.4	93.0	7320	4	US-08-367-685-2	Sequence 2, Appli
19	1131.4	93.0	7320	5	PCT-US91-07141-2	Sequence 2, Appli
20	1131.4	93.0	7557	1	US-08-464-136-4	Sequence 4, Appli
21	1131.4	93.0	7557	2	US-08-349-131-4	Sequence 4, Appli
22	1131.4	93.0	7557	3	US-08-470-297A-4	Sequence 4, Appli
23	1131.4	93.0	7557	5	PCT-US91-07149-4	Sequence 4, Appli
24	1131.4	93.0	8118	1	US-08-464-136-5	Sequence 5, Appli
25	1131.4	93.0	8118	2	US-08-349-131-5	Sequence 5, Appli
26	1131.4	93.0	8118	3	US-08-470-297A-5	Sequence 5, Appli
27	1131.4	93.0	8118	5	PCT-US91-07149-5	Sequence 5, Appli

C 28	1131	92.9	7394	1	US-08-440-787A-6	Sequence 6, Appli
C 29	1131	92.9	7394	4	US-08-367-685-6	Sequence 6, Appli
C 30	1131	92.9	7394	5	PCT-US91-07141-6	Sequence 6, Appli
C 31	1131	92.9	7409	1	US-08-440-787A-4	Sequence 4, Appli
C 32	1131	92.9	7409	4	US-08-367-685-4	Sequence 4, Appli
C 33	1131	92.9	7409	5	PCT-US91-07141-4	Sequence 4, Appli
C 34	1131	92.9	7445	1	US-08-464-136-1	Sequence 1, Appli
C 35	1131	92.9	7445	1	US-08-440-787A-3	Sequence 3, Appli
C 36	1131	92.9	7445	2	US-08-349-131-1	Sequence 1, Appli
C 37	1131	92.9	7445	4	US-08-470-297A-1	Sequence 1, Appli
C 38	1131	92.9	7445	4	US-08-367-685-3	Sequence 3, Appli
C 39	1131	92.9	7445	5	PCT-US91-07149-1	Sequence 3, Appli
C 40	1131	92.9	7445	5	PCT-US91-07149-1	Sequence 3, Appli
C 41	1131	92.9	7729	1	US-08-464-136-3	Sequence 3, Appli
C 42	1131	92.9	7729	2	US-08-349-131-3	Sequence 3, Appli
C 43	1131	92.9	7729	3	US-08-470-297A-3	Sequence 3, Appli
C 44	1131	92.9	7729	5	PCT-US91-07149-3	Sequence 3, Appli
C 45	846.8	69.6	7652	1	US-07-590-988A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-726-462B-1
; Sequence 1, Application US/08726462B
; Patent No. 5800996
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,462B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462B-1

Query Match 100.0%; Score 1217; DB 1; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60
DB 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

QY 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTCACACAA 120
DB 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTCACACAA 120

QY 121 CATAGAGCGGGAACATTAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAAGTAACTAC 180
DB 121 CATAGAGCGGGAACATTAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAAGTAACTAC 180

QY 181 ATTAATTCGGTTCGCTCAGCTGCCGCTTCCAGTCCGGAAACCTGTGTCGACGCTGCA 240
DB 181 ATTAATTCGGTTCGCTCAGCTGCCGCTTCCAGTCCGGAAACCTGTGTCGACGCTGCA 240

QY 241 TTAATGAATCGGCACACCGCGGGGAGAGCGGTTTGGCTATTTGGCGCCAGGGTGGTTT 300
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QY 301 TTCTTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCCCTTCCAGCTGCGGCTGAGAGA 360
DB 301 TTCTTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCCCTTCCAGCTGCGGCTGAGAGA 360

QY 361 GTTGCAGAACGGTTCACGCTGTTTTCGCCAGCAGCGGAAATCTGTTGATGTTGG 420
DB 361 GTTGCAGAACGGTTCACGCTGTTTTCGCCAGCAGCGGAAATCTGTTGATGTTGG 420

QY 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGT 480
DB 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGT 480

QY 481 TGTTCAGTTTGAACAGAGTCCACCTATTAAAGAACTGACCTCCACGCTCAAGGCGG 540
DB 481 TGTTCAGTTTGAACAGAGTCCACCTATTAAAGAACTGACCTCCACGCTCAAGGCGG 540

QY 541 AAAACCGTCTATCAGGCGGATGCCACCTACGTTGAACCAATCAAGTTTTTTT 600
DB 541 AAAACCGTCTATCAGGCGGATGCCACCTACGTTGAACCAATCAAGTTTTTTT 600

QY 601 GGGTTCAGGTCGCTGATGAGCTAAATCGGACCTTAAGGGAGCCCCCGATTTAGAGC 660
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QY 661 TTGACGGGAAAGCGCGGAACTGGCGAGAAAGGAAAGGAAAGGAGGAGCGG 720
DB 661 TTGACGGGAAAGCGCGGAACTGGCGAGAAAGGAAAGGAAAGGAGGAGCGG 720

QY 721 CGCTAGGCGCTGCGAGTGTAGGCTGACGCTGCGGCTAACCAACACCGCCGCGCT 780
DB 721 CGCTAGGCGCTGCGAGTGTAGGCTGACGCTGCGGCTAACCAACACCGCCGCGCT 780

QY 781 TAATGCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGCAGCAGCTAATAGCTGTTT 840
DB 781 TAATGCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGCAGCAGCTAATAGCTGTTT 840

QY 841 CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGGCGGATTAAGGAGTTTACAGAGGA 900
DB 841 CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGGCGGATTAAGGAGTTTACAGAGGA 900

QY 901 ACGGTACGCGCAATCTTCAGAGTCTTTTATTAATCAGTGAAGCCAGGAGGAGGAG 960
DB 901 ACGGTACGCGCAATCTTCAGAGTCTTTTATTAATCAGTGAAGCCAGGAGGAGGAG 960

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DB 961 TCTGTCCATCAGCAATTAACGCTGTAGCAATCTTCTTATTAATAGTAATTAACATCAC 1020

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DB 1021 TTGCGCTGAGTAGAAGAACTCAAACTATCGGCTTGTGTTGTAATATCCAGCAATATTAC 1080

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DB 1081 CGCCAGCCTTGCACACAGGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCG 1140

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DB 1141 TCTGAATGATTTATTTACATTTGCAGATTCCACAGTTCACAGGAGTAAATAAAGGGA 1200

QY 1201 CATTTGCGCAACAGAG 1217

DB 1201 CATTTGCGCAACAGAG 1217

RESULT 2

US-08-642-330-1

; Sequence 1, Application US/08642330

; Patent No. 5863727

; GENERAL INFORMATION:

; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems

; APPLICANT: Division

; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED

; TITLE OF INVENTION: FLUORESCENCE

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David J. Weitz, Haynes & Davis

; STREET: 2180 Sand Hill Road, Suite 310

; CITY: Menlo Park

; STATE: California

; COUNTRY: USA

; ZIP: 94025-6935

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0

; SOFTWARE: Wordperfect for Windows 6.0.

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/642,330

; FILING DATE:

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: David J. Weitz

; REGISTRATION NUMBER: 38,362

; REFERENCE/DOCKET NUMBER: PELM4303

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 233-0188

; TELEFAX: (415) 233-1129

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1217 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-642-330-1

Query Match 100.0%; Score 1217; DB 2; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

DB 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

QY 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTCACACAA 120

DB 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTCACACAA 120

121 CATACAGCCGGAAGCATAAAGTGTAAAGCCTGGGTGCTATGAGTGAAGTCACTAC 180
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181 ATTAATGCGTTGCGCTACTCGCCGCTTTCAGTCGGGAAACCTGCTGCGCCAGCTGCA 240
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301 TTTCTTTTACCACTGAGAGCGGCAACGCTGATGCTTCCCTTCACCGCTGCGCTGAGAGA 360
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481 TGTTCAGTTTGAACAAGAGTCCACTATTAAGAGAGTGGACTTCCCAAGTCAAGGGCG 540
541 AAAAAACGCTATACAGGGCGATGCGGCTACGCTGAAACCATCACCCAAATCAAGTTTTT 600
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601 GGGGTCGAGTGCCTAAAGCACTAAATCGAAGCCCTAAAGGGAGCCCGATTTAGAGC 660
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841 CCTGTTGGATCAGAGCGGAGCTAAACAGGAGGCGGATTAAGGGATTTTAGACAGGA 900
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961 TCTGTCCATCAGCAAAATTAACGCTGTAGCAATCTTCTTGTAGTAAATACATCAC 1020
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1081 CGCCAGCAATTCGAACAGGAAAGAGCTCATGGAATACCTACATTTTGAACGCTCAATCG 1140
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1141 TCTGAATGGATTTTACATTTGGAGATTTACAGTACAGGAGGAGTAAAGAGGA 1200
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QY 1201 CATTCTGCCAACAGAG 1217
Db 1201 CATTCTGCCAACAGAG 1217
RESULT 3
US-09-046-203-1
; Sequence 1, Application US/09046203
; Patent No. 5945526
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-746
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-046-203-1

Query Match 100.0%; Score 1217; DB 2; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAAGCTTGCAATGCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
Db 1 GCCAAGCTTGCAATGCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
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Db 61 GTAATCATGCTCATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCAAAATTCACACAA 120
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481 TGTTCAGTTTGGAAACAGAGTCCACTATTAAGAACGCTGACCTCCAAACGTCAGAGGCG 540
541 AAAAACGCTTATCAGGCGGATGCCCACTACGTTGAACCATCACCCCAATCAAGTTT 600
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841 CTTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGGCGGATTAAGGATTTAGACAGGA 900
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1021 TTGCTTCAGTGAAGAACTCAAACTATCGGCTTGTGTTGTAATATCCAGAACATATTAC 1080
1021 TTGCTTCAGTGAAGAACTCAAACTATCGGCTTGTGTTGTAATATCCAGAACATATTAC 1080
1081 CGCCAGCCATTGACAGGAAACGCTCATGGAATACCTACATTTTTCAGCTCAATCG 1140
1081 CGCCAGCCATTGACAGGAAACGCTCATGGAATACCTACATTTTTCAGCTCAATCG 1140
1141 TCTGAATGGATTTTACATTTGGCAGATTCACCACTGACACCAACCAAGTAAATGAGGGA 1200
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1201 CATTTGCGCAACAGAG 1217

RESULT 4

US-09-272-104-1
; Sequence 1, Application US/09272104
; Patent No. 6145434
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: METHOD FOR DETECTING
; TITLE OF INVENTION: OLIGONUCLEOTIDES USING ENERGY TRANSFER DYES WITH LONG STOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSER: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,104
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-272-104-1

Query Match 100.0%; Score 1217; DB 3; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAAGCTTCATCCCTGCGAGTCGACTCTAGAGATCCCCGGGTACCGGAGCTCGAATTC 60
Db 1 GCCAAGCTTCATCCCTGCGAGTCGACTCTAGAGATCCCCGGGTACCGGAGCTCGAATTC 60
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QY 721 CGCTAGGCGCTGCAAGCTGATAGGCTGACGCTGCGCTTAACACACACCGCGCGCT 780
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QY 781 TAATGCGCGCTACAGGCGCGTACTATGTTGCTTTCAGGAGCAGCTATACGTCGTT 840
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QY 841 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTTAGACAGA 900
Db 841 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTTAGACAGA 900
QY 901 ACGGTACGCCAGAACTCTTGAAGTGTATTAATCAAGTACGAGGCGGATTAAGAGAG 960
Db 901 ACGGTACGCCAGAACTCTTGAAGTGTATTAATCAAGTACGAGGCGGATTAAGAGAG 960
QY 961 TCTGTCATACGCAAAATTAACCGTTGAGCAATCTCTTTGATTAGTAATACATCAC 1020
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Db 1201 CATTCCTGCGCAACAGAG 1217

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RESULT 5
US-09-272-097-1
; Sequence 1, Application US/09272097
; Patent No. 6335440
; GENERAL INFORMATION:
; APPLICANT: PE Corporation (NY)
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES USING
; ENERGY TRANSFER DYES WITH LONG STROKE SHIFT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Word 97
; ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,097
; FILING DATE: 18-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 493-9300
; TELEFAX: (650) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-272-097-1

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Query Match 100.0%; Score 1217; DB 4; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTCATGCTGCTGAGGTCGAGTCCCGGCTACCGAGCTCGAATTC 60
Db 1 GCCAAGCTTCATGCTGCTGAGGTCGAGTCCCGGCTACCGAGCTCGAATTC 60
QY 61 GTAATCATGCTATAGCTGTTCTGCTGTGAAATTTATCCGCTCACAATTCACACAA 120
Db 61 GTAATCATGCTATAGCTGTTCTGCTGTGAAATTTATCCGCTCACAATTCACACAA 120
QY 121 CATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTACGCTACAC 180
Db 121 CATACGAGCGGAGCATAAAGTGTAAAGCTGGGGTGCCTTAATGAGTACGCTACAC 180
QY 181 ATTAATTCGCTGCGCTCACTGCCGCTTCCAGTCGGGAACCTGCTGTCACAGCTGCA 240
Db 181 ATTAATTCGCTGCGCTCACTGCCGCTTCCAGTCGGGAACCTGCTGTCACAGCTGCA 240

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Qy	241	TTAATGAATCGGCCAACGGCGGGGAGAGCGCGTTTCGCGTATTGGGCGCCACGGGTGGTTT	300
Db	241	TTAATGAATCGGCCAACGGCGGGGAGAGCGCGTTTCGCGTATTGGGCGCCACGGGTGGTTT	300
Qy	301	TTCTTTTTCACCACTAGAGCGGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGA	360
Db	301	TTCTTTTTCACCACTAGAGCGGGCAACAGCTGATTGCCCTTCACCGCCTGGCCCTGAGAGA	360
Qy	361	GTTCGAGCAAGCGGTCCACGCTGGTTTGCCCGCAGCAGCGGAAAAATCTGTGTTGATGGTGG	420
Db	361	GTTCGAGCAAGCGGTCCACGCTGGTTTGCCCGCAGCAGCGGAAAAATCTGTGTTGATGGTGG	420
Qy	421	TTCCGAAATCGCGCAAAATCCCTTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT	480
Db	421	TTCCGAAATCGCGCAAAATCCCTTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT	480
Qy	481	TGTTCCAGTTTGACAAGAGTCCACTATTAAAGAACGTGGACTCCAAACGTCAAAGGCGC	540
Db	481	TGTTCCAGTTTGACAAGAGTCCACTATTAAAGAACGTGGACTCCAAACGTCAAAGGCGC	540
Qy	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGCTTTT	600
Db	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGCTTTT	600
Qy	601	GGGTCGAGTCCGTTAAGCACTAAATCGGAACCTTAAAGGAGGCCCGGATTTAGAGC	660
Db	601	GGGTCGAGTCCGTTAAGCACTAAATCGGAACCTTAAAGGAGGCCCGGATTTAGAGC	660
Qy	661	TTGACGGGGAACCGCGCAACGTTGCGGAGAAAGGAAGGAACGAAAGAGCAGCGGG	720
Db	661	TTGACGGGGAACCGCGCAACGTTGCGGAGAAAGGAAGGAACGAAAGAGCAGCGGG	720
Qy	721	CGCTAGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAAACCAACACCCCGCGCGCT	780
Db	721	CGCTAGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAAACCAACACCCCGCGCGCT	780
Qy	781	TAATCGCGCGCTACAGGGCGCTACTATCGTTTGTAGGACGACGTATAACGTGCTTT	840
Db	781	TAATCGCGCGCTACAGGGCGCTACTATCGTTTGTAGGACGACGTATAACGTGCTTT	840
Qy	841	CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGCGATTAAAGGGATTTTAGACAGGA	900
Db	841	CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGCGCGATTAAAGGGATTTTAGACAGGA	900
Qy	901	ACGGTACGCCAGAACTCTTGAGAACTGTTTTATATACGTGAGCGCACCGAGTAAAGAG	960
Db	901	ACGGTACGCCAGAACTCTTGAGAACTGTTTTATATACGTGAGCGCACCGAGTAAAGAG	960
Qy	961	TCTGTCCATCAGGCAAAATTAACCGTTGTAGCAATACTCTTTGATTAGTAAATCAATCAC	1020
Db	961	TCTGTCCATCAGGCAAAATTAACCGTTGTAGCAATACTCTTTGATTAGTAAATCAATCAC	1020
Qy	1021	TTGCCTGAGTAGAAGAACTCAAACTATCGGCCTTGGTGTAAATATACAGAACAAATATAC	1080
Db	1021	TTGCCTGAGTAGAAGAACTCAAACTATCGGCCTTGGTGTAAATATACAGAACAAATATAC	1080
Qy	1081	GGCAGAGCAATGGAACAGGAAAAACCGCTCATGSAATACCTACATTTTGACGCTCAATCG	1140
Db	1081	GGCAGAGCAATGGAACAGGAAAAACCGCTCATGSAATACCTACATTTTGACGCTCAATCG	1140
Qy	1141	TCTCAATGGGATTTATTTACATTTGGCAGATTTACCAGTACACGACCAAGTAATAAGGGA	1200
Db	1141	TCTCAATGGGATTTATTTACATTTGGCAGATTTACCAGTACACGACCAAGTAATAAGGGA	1200
Qy	1201	CATTCTGCCCAACAGAG	1217
Db	1201	CATTCTGCCCAACAGAG	1217

RESULT 6

RESULT 6
US-08-440-787A-1/C

US-08-440-787A-1/C
: Sequence 1, Application US/08440787A

Sequence 1, Application No. 5770434

```

: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: TITLE OF INVENTION: Soluble Peptides Having Constrained,
: TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
: TITLE OF INVENTION: Same.
: NUMBER OF SEQUENCES: 174
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440.787A
: FILING DATE: 15-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/978,893
: FILING DATE: 10-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-IX 1586
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7294 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: circular
: US-08-440-787A-1

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Query Match 94.6%; Score 1150.8; DB 1; Length 7294;
Best Local Similarity 99.8%; Pred. NO. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0;

Qy	64	ATCATGGTCA	TAGCTGTT	TTCCTGTGTG	AAATTTGTTAT	CCGCTCACA	ATTTCCACACA	CAAT	123
Db	6226	ATCCTGGTCA	TAGCTGTT	TTCCTGTGTG	AAATTTGTTAT	CCGCTCACA	ATTTCCACACA	CAAT	6167
Qy	124	ACGAGCCGGA	AGCATAAAG	TGTAAAGCCT	TGGGGTGCC	TAAAGTGTAA	TGAGTGA	GAGTCA	183
Db	6166	ACGAGCCGGA	AGCATAAAG	TGTAAAGCCT	TGGGGTGCC	TAAAGTGTAA	TGAGTGA	GAGTCA	6107
Qy	184	AATTCGCTTG	GGCTCAC	TGCCCGCT	TTTCCAGT	CGGGAAAC	CTCTCGT	GCCAGCTG	243
Db	6106	AATTCGCTTG	GGCTCAC	TGCCCGCT	TTTCCAGT	CGGGAAAC	CTCTCGT	GCCAGCTG	6047
Qy	244	ATGAATCGGC	CAACCGCG	GGGAGAGCG	GTTTGCGTAT	TGGCGCC	ACAGSGTGG	TTTTTC	303
Db	6046	ATGAATCGGC	CAACCGCG	GGGAGAGCG	GTTTGCGTAT	TGGCGCC	ACAGSGTGG	TTTTTC	5987
Qy	304	TTTTTACCAC	TGAGACGG	GCACACGT	GATTCGCC	TTACACGC	CTGGCCCT	GAGAGAGTT	363
Db	5986	TTTTTACCAC	TGAGACGG	GCACACGT	GATTCGCC	TTACACGC	CTGGCCCT	GAGAGAGTT	5927
Qy	364	GCAGCAAGCG	GTCCAC	CGCTGTTT	TGCCCC	CAGCAGGCG	AAAAATC	CTCTTTGAT	423
Db	5926	GCAGCAAGCG	GTCCAC	CGCTGTTT	TGCCCC	CAGCAGGCG	AAAAATC	CTCTTTGAT	5867
Qy	424	CGAAATCGGC	AAAAATC	CCCTTATA	ATAATCA	AAAGAAAT	TAGCCCG	GAGATAG	483
Db	5866	CGAAATCGGC	AAAAATC	CCCTTATA	ATAATCA	AAAGAAAT	TAGCCCG	GAGATAG	5807


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QY 484 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 5747
QY 544 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCACCAATCAAGTTTGGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCACCAATCAAGTTTGGG 5687
QY 604 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 663
Db 5686 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGGAAAGGAGGAGGCGGCG 723
Db 5626 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGGAAAGGAGGAGGCGGCG 5567
QY 724 TAGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAAACACACACACCGCGCGCTTAA 783
Db 5566 TAGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAAACACACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGGTATACGTGCTTCT 843
Db 5506 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGGTATACGTGCTTCT 5447
QY 844 CTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAGGGATTTAGACAGGAACG 903
Db 5446 CTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAGGGATTTAGACAGGAACG 5387
QY 904 GTACGCGAGATCTTCAAGAGTGTATTAATCACTGAGCGCCACCGAGTAAAGAGTCT 963
Db 5386 GTACGCGAGATCTTCAAGAGTGTATTAATCACTGAGCGCCACCGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAATTAACCGTTGTAGCAATCTCTTTGATAGTAATTAACATCACTTG 1023
Db 5326 GTCCATCAGCAATTAACCGTTGTAGCAATCTCTTTGATAGTAATTAACATCACTTG 5267
QY 1024 CTTGAGTAGAGAGTCAACTATCGCTTGTGTAATTAACAGAACTAATTAACCGC 1083
Db 5266 CTTGAGTAGAGAGTCAACTATCGCTTGTGTAATTAACAGAACTAATTAACCGC 5207
QY 1084 CAGCCATTCAGCAAGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 1143
Db 5206 CAGCCATTCAGCAAGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 5147
QY 1144 GAAATGATTTATACATTCGAGATTCACAGTCACAGCAGCAGTAAATAAGGAGAT 1203
Db 5146 GAAATGATTTATACATTCGAGATTCACAGTCACAGCAGCAGTAAATAAGGAGAT 5087
QY 1204 TCTGGCCAAACAGAG 1217
Db 5086 TCTGGCCAAACAGAG 5073

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RESULT 7
US-08-440-787A-5/c
; Sequence 5, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-440-787A-5

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Query Match 94.6%; Score 1150.8; DB 1; Length 7294;
Best Local Similarity 99.8%; Pred. No. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACAAATCCACACAAAT 123
Db 6226 ATCTGTTGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACAAATCCACACAAAT 6167
QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGGCTGCTAATCAGTGAGCTAACTCACATT 183
Db 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGGTGGCTGCTAATCAGTGAGCTAACTCACATT 6107
QY 184 AATTGCTGTTGCTCACTACCTCCCGCTTTCCAGTCCGGAACCTGTCGTGCCAGCTGCATTA 243
Db 6106 AATTGCTGTTGCTCACTACCTCCCGCTTTCCAGTCCGGAACCTGTCGTGCCAGCTGCATTA 6047
QY 244 ATGAATCGGCAACCGCGGGGAGAGCGGTTTGGTATTGGGCGCAGGGTGGTTTTC 303
Db 6046 ATGAATCGGCAACCGCGGGGAGAGCGGTTTGGTATTGGGCGCAGGGTGGTTTTC 5987
QY 304 TTTTCCAGCTGAGAGCGGCAACAGCTGATGCTTCCAGTCCAGCTGAGAGATT 363
Db 5986 TTTTCCAGCTGAGAGCGGCAACAGCTGATGCTTCCAGTCCAGCTGAGAGATT 5927
QY 364 GCAGCAAGGGGTCCAGCTGTTTGGCCCGAGGCGGAAATCCTGTTGATGTTGTTTC 423
Db 5926 GCAGCAAGGGGTCCAGCTGTTTGGCCCGAGGCGGAAATCCTGTTGATGTTGTTTC 5867
QY 424 CGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGT 483
Db 5866 CGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCCACTATTAAGACGTGGACTCCAAAGTCAAAGGCGGAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCCACTATTAAGACGTGGACTCCAAAGTCAAAGGCGGAA 5747
QY 544 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCACCAATCAAGTTTGGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCACCAATCAAGTTTGGG 5687
QY 604 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 663
Db 5686 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGGAAAGGAAAGGAGGAGGCGGCG 723
Db 5626 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGGAAAGGAAAGGAGGAGGCGGCG 5567

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QY 724 TAGGGCGCTGCGAAGTGTAGCGGTACGCTGCGCGTAAACACACACCGCGCGCTTAA 783
Db 5566 TAGGGCGCTGCGAAGTGTAGCGGTACGCTGCGCGTAAACACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGGTATAAGTGTCTTCT 843
Db 5506 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGGTATAAGTGTCTTCT 5447
QY 844 CTTTGAATCAGAGCGGCGGTAAACAGAGGCGCGATTAAGGGATTTTAGACAGGAACG 903
Db 5446 CTTTGAATCAGAGCGGCGGTAAACAGAGGCGCGATTAAGGGATTTTAGACAGGAACG 5387
QY 904 GTACCGCGAGACTCTGAGAGCTGTTTATATATCAGTGAAGCGACCGAGTAAAGTCT 963
Db 5386 GTACCGCGAGACTCTGAGAGCTGTTTATATATCAGTGAAGCGACCGAGTAAAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTGTAGCAATCTTTGATTACTAATAACATCACTTG 1023
Db 5326 GTCCATCAGCAAAATTAACCGTGTAGCAATCTTTGATTACTAATAACATCACTTG 5267
QY 1024 CTTGAGTAGAAGACTCAAACTATCGGCGTGTGCTGTTATATCCAGAAATATTACCGC 1083
Db 5266 CTTGAGTAGAAGACTCAAACTATCGGCGTGTGCTGTTATATCCAGAAATATTACCGC 5207
QY 1084 CAGCATTTGCAACAGGAAACCGCTCATGGAAATACCTACATTTTGAGCGCTCAATCGTCT 1143
Db 5206 CAGCATTTGCAACAGGAAACCGCTCATGGAAATACCTACATTTTGAGCGCTCAATCGTCT 5147
QY 1144 GAAATGGATTATTACATTTGCGAGATTCAACAGTCAACAGGCGGTATTAAGGGAGAT 1203
Db 5146 GAAATGGATTATTACATTTGCGAGATTCAACAGTCAACAGGCGGTATTAAGGGAGAT 5087
QY 1204 TCTGGCCAAACAGAG 1217
Db 5086 TCTGGCCAAACAGAG 5073

RESULT 8

US-08-367-685-1/c
; Sequence 1, Application US/08367685
; Patent No. 6258530
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; NUMBER OF INVENTION: RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,685
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,494
; FILING DATE:
; APPLICATION NUMBER: US/07/767,436
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-367-685-1

Query Match 94.6%; Score 1150.8; DB 4; Length 7294;
Best Local Similarity 99.8%; Pred. No. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATCGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAAATCCACACAACAT 123
Db 6226 ATCTCGTGTATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAAATCCACACAACAT 6167
QY 124 ACAGCGCGGAAGCATAAAGTGTAAAGCCTGCGGTGCTTAATGAGTGAGCTTAACCTCACATT 183
Db 6166 ACAGCGCGGAAGCATAAAGTGTAAAGCCTGCGGTGCTTAATGAGTGAGCTTAACCTCACATT 6107
QY 184 AATTGGCTTGGCTCACTGCCGCTTTCCAGTCGGGAAACCTTCGTCGCCAGTGCATTA 243
Db 6106 AATTGGCTTGGCTCACTGCCGCTTTCCAGTCGGGAAACCTTCGTCGCCAGTGCATTA 6047
QY 244 ATGAATCGGCCAACGCGGGAGAGCGGTTTTCGCTATTGGCGCCAGCGGTGTTTTC 303
Db 6046 ATGAATCGGCCAACGCGGGAGAGCGGTTTTCGCTATTGGCGCCAGCGGTGTTTTC 5987
QY 304 TTTTCACCAGTCAGAGCGGCAACAGCTGATTGCCCTTCACCGCTGCGCCCTGAGAGAGTT 363
Db 5986 TTTTCACCAGTCAGAGCGGCAACAGCTGATTGCCCTTCACCGCTGCGCCCTGAGAGAGTT 5927
QY 364 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGAGCGGAAATCTCTTTGATGGTGTTC 423
Db 5926 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGAGCGGAAATCTCTTTGATGGTGTTC 5867
QY 424 CGAAATCGGCAAAATCCCTTATATAATCAAAAGATAGCCGAGATAGGCTGAGTGTCT 483
Db 5866 CGAAATCGGCAAAATCCCTTATATAATCAAAAGATAGCCGAGATAGGCTGAGTGTCT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACCTGGACTCCAACGTCGTCGCGGAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACCTGGACTCCAACGTCGTCGCGGAA 5747
QY 544 AACGCTCTATCAGGCGGATGCGCCACTAGTCAACCATCACCCCAATCAAGTTTTCGG 603
Db 5746 AACGCTCTATCAGGCGGATGCGCCACTAGTCAACCATCACCCCAATCAAGTTTTCGG 5687
QY 604 GTCAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGAGCGCCCGATTTAGAGCTTG 663
Db 5686 GTCAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGAGCGCCCGATTTAGAGCTTG 5627
QY 664 ACGGGAAAGCGCGCAACGTTGGCGAGAAAGAGGGAAGAAAGCGAGCGGCGC 723
Db 5626 ACGGGAAAGCGCGCAACGTTGGCGAGAAAGAGGGAAGAAAGCGAGCGGCGC 5567
QY 724 TAGGCGCTGCGCAAGTGTAGCGGTACCGCTGCGGTAAACCAACACCGCGCGCTTAA 783
Db 5566 TAGGCGCTGCGCAAGTGTAGCGGTACCGCTGCGGTAAACCAACACCGCGCGCTTAA 5507
QY 784 TGGCCCGCTACAGGCGGCTAAACAGGCGCGGATTAAGGGATTTTAGACAGGAACG 903
Db 5446 CTTTGAATCAGAGCGGCGGTAAACAGGCGCGGATTAAGGGATTTTAGACAGGAACG 5387
QY 904 GTACCGCGAGACTCTGAGAGTGTGTTTATATCAGTGAAGCGACCGAGTAAAGTCT 963
Db 5386 GTACCGCGAGACTCTGAGAGTGTGTTTATATCAGTGAAGCGACCGAGTAAAGTCT 5327

Db 5146 GAATGGATTATTACATTGGCAGATTACCAAGTCCACAGCAGCAATATAAAGGACAT 5087

Qy 1204 TCTGGCCACAGAG 1217

Db 5086 TCTGGCCACAGAG 5073

RESULT 10

PCT-US91-07141-1/c

; Sequence 1, Application PC/TUS9107141

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: RANDOMIZED PEPTIDES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: United States

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/07141

; FILING DATE: 19910927

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P31 9072

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7294 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: both

; TOPOLOGY: circular

PCT-US91-07141-1

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;

Best Local Similarity 99.8%; Pred. No. 1e-246;

Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 ATCATGGTCATAGCTGTTTCTGTTGTAAGTGTATTCGCTCACAATTCCACACAACAT 123

Db 6226 ATCTGGTGTATAGCTGTTTCTGTTGTAAGTGTATTCGCTCACAATTCCACACAACAT 6167

Qy 124 ACAGCGCGGAAGCATAAAGTGTAAAGCTGGGGTGTATTCGCTCACAATTCCACACAACAT 183

Db 6166 ACAGCGCGGAAGCATAAAGTGTAAAGCTGGGGTGTATTCGCTCACAATTCCACACAACAT 6107

Qy 184 AATTGGGTTGCGCTCACTGCGCCGCTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTA 243

Db 6106 AATTGGGTTGCGCTCACTGCGCCGCTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTA 6047

Qy 244 ATCAATCGCCACACGCGCGGGAGAGCGGTTTGGGTATTTGGGCGCGAGGTTTTC 303

Db 6046 ATCAATCGCCACACGCGCGGGAGAGCGGTTTGGGTATTTGGGCGCGAGGTTTTC 5987

Qy 304 TTTTCCACAGTACAGCGGCAACAGCTGATTGCCCTTCCAGCTGCGCTGAGAGATT 363

Db 5986 TTTTCCACAGTACAGCGGCAACAGCTGATTGCCCTTCCAGCTGCGCTGAGAGATT 5927

Qy 364 GCAGCAGCGGTCACAGCTGGTTTGGCCCGCAGCAGGAAATCCTGTTGATGGTGTTC 423

Db 5087 TCTGGCCCAACAGAG 5073

Db 5926 GCAGCAAGCGGTCCACGCTGGTTTGGCCCGCAGCGCAAAATCCTGTTTGATGTTGGTTC 5867

Qy 424 CGAAATCGGCAAAATCCCTTTATAATCAAAAGATATCCCGAGATAGGTTGAGTTGT 483

Db 5866 CGAAATCGGCAAAATCCCTTTATAATCAAAAGATATCCCGAGATAGGTTGAGTTGT 5807

Qy 484 TCCAGTTTGGCAACAAGAGTCCACTATTAAAGAACGTTGGACTCCAACTCAAGGGCGGAAA 543

Db 5806 TCCAGTTTGGCAACAAGAGTCCACTATTAAAGAACGTTGGACTCCAACTCAAGGGCGGAAA 5747

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Db 5746 AACCGTCTATCAGGGCGATGGCCCACTACCTGAACCATCACCCAAATCAAGTTTGGG 5687

Qy 604 GTCGAGTGGCGTAAAGCACTAAATCGGAACCTTAAAGGAGGCCCGCGATTAGAGCTTG 663

Db 5686 GTCGAGTGGCGTAAAGCACTAAATCGGAACCTTAAAGGAGGCCCGCGATTAGAGCTTG 5627

Qy 664 ACGGGAAAAGCGCGCAACGTGCGAGAAAGGAGGAAGCAAGCAAGCAAGGAGCGGCGC 723

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Db 5566 TAGGGCGTGGCAAGTGTAGCGGTACGCTGCGCTAAACACACACCCCGCGCTTAA 5507

Qy 784 TCGCGCGCTACAGGGCGGCTACTATGTTGCTTTGACGACGATATAAGCTGTTTCT 843

Db 5506 TCGCGCGCTACAGGGCGGCTACTATGTTGCTTTGACGACGATATAAGCTGTTTCT 5447

Qy 844 CTTTGGAAATCAGAGGGGAGCTAAACAGAGGCGCGATTAAAGGATTATAGACAGGAACG 903

Db 5446 CTTTGGAAATCAGAGGGGAGCTAAACAGAGGCGCGATTAAAGGATTATAGACAGGAACG 5387

Qy 904 GTACGCCAGATCTTTGAGAAGTGTATTAATACAGTGAGGCGCACCGAGTAAAGAGTCT 963

Db 5386 GTACGCCAGATCTTTGAGAAGTGTATTAATACAGTGAGGCGCACCGAGTAAAGAGTCT 5327

Qy 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTCTTTGATTAGTAATAACATCATCTG 1023

Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTCTTTGATTAGTAATAACATCATCTG 5267

Qy 1024 CTTGAGTAGAAGACTCAAACTATCGGCTTGTGTTGTAATATCCAGCAACAATATACCGC 1083

Db 5266 CTTGAGTAGAAGACTCAAACTATCGGCTTGTGTTGTAATATCCAGCAACAATATACCGC 5207

Qy 1084 CAGCCATTGCACACAGAAAACGCTCATGGAAATACCTACATTTTACGCTCAATCGTCT 1143

Db 5206 CAGCCATTGCACACAGAAAACGCTCATGGAAATACCTACATTTTACGCTCAATCGTCT 5147

Qy 1144 GAAATGGATTATTTACATTGGCAGATTCCACAGTCCACAGCAGCAGTAAATAAAGGACAT 1203

Db 5146 GAAATGGATTATTTACATTGGCAGATTCCACAGTCCACAGCAGCAGTAAATAAAGGACAT 5087

Qy 1204 TCTGGCCCAACAGAG 1217

Db 5086 TCTGGCCCAACAGAG 5073

RESULT 11

PCT-US91-07141-5/c

; Sequence 5, Application PC/TUS9107141

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: RANDOMIZED PEPTIDES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: United States

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; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07141
; FILING DATE: 19910927
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Both
; TOPOLOGY: circular
; PCT-US91-07141-5

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Query Match 94.68; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.98; Pred. No. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTCATAGCTGTTTCCCTGTGAAATGTTATCCGCTCAAAATTCACACAACAT 123
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QY 124 ACAGCCGGAAGCATAAAGTGTAAAGCCTGGGTGCCTAATGAGTGAGCTAACTACAT 183
DB 6166 ACAGCCGGAAGCATAAAGTGTAAAGCCTGGGTGCCTAATGAGTGAGCTAACTACAT 6107

QY 184 AATTGCTGTCGCTACGCTCCGCTTTCCAGTCGGGAACCTGTCGTGCAGCTGCATTA 243
DB 6106 AATTGCTGTCGCTACGCTCCGCTTTCCAGTCGGGAACCTGTCGTGCAGCTGCATTA 6047

QY 244 ATGAATCGCCCAACCGCGGGAGAGCGGTTTGGCTATTGGCGCCAGGGGTTTTC 303
DB 6046 ATGAATCGCCCAACCGCGGGAGAGCGGTTTGGCTATTGGCGCCAGGGGTTTTC 5987

QY 304 TTTTCACAGTGAGAGGCGCAACAGCTGATTCGCCCTTACGCCCTGGCCCTGAGAGATT 363
DB 5986 TTTTCACAGTGAGAGGCGCAACAGCTGATTCGCCCTTACGCCCTGGCCCTGAGAGATT 5927

QY 364 GCAGCAAGCGTCCAGCTGTTTCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 423
DB 5926 GCAGCAAGCGTCCAGCTGTTTCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 5867

QY 424 CGAAATCGCCAAATCCCTTATTAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTGT 483
DB 5866 CGAAATCGCCAAATCCCTTATTAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTGT 5807

QY 484 TCCAGTTGGACACAAGATCCACTATTAAAGACGTGGACTCCAAGTCAAGGGCGAA 543
DB 5806 TCCAGTTGGACACAAGATCCACTATTAAAGACGTGGACTCCAAGTCAAGGGCGAA 5747

QY 544 AACCGTCTATCAGGGCGATGGCCCTACGTGAACCATCACCAAAATCAAGTTTGTGG 603
DB 5746 AACCGTCTATCAGGGCGATGGCCCTACGTGAACCATCACCAAAATCAAGTTTGTGG 5687

QY 604 GTCAGGTCCTGTAAGCACTAAATCGGAACCTTAAAGGAGCCGCCCGATTTAGAGCTTG 663
DB 5686 GTCAGGTCCTGTAAGCACTAAATCGGAACCTTAAAGGAGCCGCCCGATTTAGAGCTTG 5627

QY 664 ACAGGGAAGCCGGCGAAGCTGGCGAAGAGGAGGAAGAGCAAGAGCGGGCGC 723
DB 5626 ACAGGGAAGCCGGCGAAGCTGGCGAAGAGGAGGAAGAGCAAGAGCGGGCGC 5567

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QY 724 TAGGGCGTGCAGAGTGTAGCGGTACGCTGCGCTAAACACACACACCCCGCGCTTAA 783
DB 5566 TAGGGCGTGCAGAGTGTAGCGGTACGCTGCGCTAAACACACACACCCCGCGCTTAA 5507

QY 784 TCGCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGTATAAGAGTCTTCC 843
DB 5506 TCGCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGTATAAGAGTCTTCC 5447

QY 844 CGTTTGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAGGGATTTTACAGAGGAG 903
DB 5446 CGTTTGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAGGGATTTTACAGAGGAG 5387

QY 904 GTACGCCAGAACTCTTGAGAAAGTGTGTTTATAATCACTGAGGCCACCGAGTAAAGAGTCT 963
DB 5386 GTACGCCAGAACTCTTGAGAAAGTGTGTTTATAATCACTGAGGCCACCGAGTAAAGAGTCT 5327

QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTAAATCAATCACTTG 1023
DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTAAATCAATCACTTG 5267

QY 1024 CCTGAGTAGAAGAACTCAAACTATCGCCCTTGTGTTAATATCCAGAACATATTACCGC 1083
DB 5266 CCTGAGTAGAAGAACTCAAACTATCGCCCTTGTGTTAATATCCAGAACATATTACCGC 5207

QY 1084 CAGCCATTCACAGAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 1143
DB 5206 CAGCCATTCACAGAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 5147

QY 1144 GAAATGGATTATTACATTTGCGAGATTTCACAGTCCAGCAGCAGCAGTAAATCAAGGGAGAT 1203
DB 5146 GAAATGGATTATTACATTTGCGAGATTTCACAGTCCAGCAGCAGCAGTAAATCAAGGGAGAT 5087

QY 1204 TCTGCGCAACAGAG 1217
DB 5086 TCTGCGCAACAGAG 5073

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RESULT 12
US-09-198-839-1/c
; Sequence 1, Application US/09198839
; Patent No. 6190908
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray S.
; TITLE OF INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MODIFIED
; FILE OF INVENTION: FILAMENTOUS PHAGE
; FILE REFERENCE: SCR21115
; CURRENT APPLICATION NUMBER: US/09/198,839
; CURRENT FILING DATE: 1998-12-24
; PRIOR APPLICATION NUMBER: PCT/US99/18207
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: 60/096,326
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a modified
; OTHER INFORMATION: filamentous phage
US-09-198-839-1

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Query Match 93.78; Score 1140.4; DB 4; Length 7083;
Best Local Similarity 99.98; Pred. No. 2e-244;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 GCTGTTTCCCTGTGAAATGTTATCCGCTCACAATTCACACAACATACGAGCGGAAG 135
DB 7083 GCTGTTTCCCTGTGAAATGTTATCCGCTCACAATTCACACAACATACGAGCGGAAG 7024

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QY 437 ATCCCTTATAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCACGTTTGGAAAC 496
Db 5854 ATCCCTTATAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCACGTTTGGAAAC 5795
QY 497 AAGAGTCCACTATTAAGAAGCTGGAATCCAAAGGCGGAAACCGTCTATCAG 556
Db 5794 AAGAGTCCACTATTAAGAAGCTGGAATCCAAAGGCGGAAACCGTCTATCAG 5735
QY 557 GCGGATGGCCACTACGTGACCATACCCCAATCAAGTTTGGGTCGAGGTGCGGT 616
Db 5734 GCGGATGGCCACTACGTGACCATACCCCAATCAAGTTTGGGTCGAGGTGCGGT 5675
QY 617 AAAGCACTAAATCGAAACCCCTAAAGGAGGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 676
Db 5674 AAAGCACTAAATCGAAACCCCTAAAGGAGGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 5615
QY 677 GCGAAGTGGGGAAGAAAGGAAGAAAGCGAAAGAGGCGGCGGTAGGCGGTGGA 736
Db 5614 GCGAAGTGGGGAAGAAAGGAAGAAAGCGAAAGAGGCGGCGGTAGGCGGTGGA 5555
QY 737 AGTGTAGCGGTACGCTGCGGCTAACCCACACACCCGCGCTTAATGCGCGGTACAG 796
Db 5554 AGTGTAGCGGTACGCTGCGGCTAACCCACACACCCGCGCTTAATGCGCGGTACAG 5495
QY 797 GCGCGTACTATGTTGCTTGGAGGACGATATAACGCTTCTCCTCGTTGGATCAGA 856
Db 5494 GCGCGTACTATGTTGCTTGGAGGACGATATAACGCTTCTCCTCGTTGGATCAGA 5435
QY 857 GCGGAGGTAACAGGAGGCGGATTAAGGATTTTAGACAGGAACGGTAGCCAGAAATC 916
Db 5434 GCGGAGGTAACAGGAGGCGGATTAAGGATTTTAGACAGGAACGGTAGCCAGAAATC 5375
QY 917 TTGAGAGTGTATTAATCAGTGAGGCGCACCGAGTAAAGAGTCTGTCCATCACGAA 976
Db 5374 TTGAGAGTGTATTAATCAGTGAGGCGCACCGAGTAAAGAGTCTGTCCATCACGAA 5315
QY 977 ATTAACCGTTGTAGCAATACCTTCTTGTATGATTAATACATCATTGCTGAGTAAAGA 1036
Db 5314 ATTAACCGTTGTAGCAATACCTTCTTGTATGATTAATACATCATTGCTGAGTAAAGA 5255
QY 1037 ACTAAACATACGCGCTTGGTGAATATCCAGAACATATACCGCGAGCCATTGCAAC 1096
Db 5254 ACTAAACATACGCGCTTGGTGAATATCCAGAACATATACCGCGAGCCATTGCAAC 5195
QY 1097 AGGAAAACGCTCATGAAATACCTACATTTTACGCTCAATCGCTGAAATGGAATTT 1156
Db 5194 AGGAAAACGCTCATGAAATACCTACATTTTACGCTCAATCGCTGAAATGGAATTT 5135
QY 1157 TACATTGSCAGATTACAGTACACAGCAGTAAATAAAGGAGACATTTGGCCCAACAGA 1216
Db 5134 TACATTGSCAGATTACAGTACACAGCAGTAAATAAAGGAGACATTTGGCCCAACAGA 5075
QY 1217 G 1217
Db 5074 G 5074

RESULT 14

US-08-349-131-2/c

; Sequence 2, Application US/08349131

; Patent No. 5871974

; GENERAL INFORMATION:

; APPLICANT: HUSE, WILLIAM D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: HETEROMERIC RECEPTORS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK

; STREET: 444 SO. FLOWER STREET, SUITE 200

; CITY: LOS ANGELES

; STATE: CALIFORNIA

; COUNTRY: UNITED STATES

; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,648
; FILING DATE:
; APPLICATION NUMBER: US/07/767,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHERYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-349-131-2

Query Match 93.0%; Score 1131.4; DB 2; Length 7317;
Best Local Similarity 99.5%; Pred. No. 2e-242;
Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 77 CTGTTTCTCTGTGAAATTTGTTATCGCTCACAAATCCACACAAATACGAGCGCGAAGC 136
Db 6214 CTCTTTGGGCTGTGAAATTTGTTATCGCTCACAAATCCACACAAATACGAGCGCGAAGC 6155
QY 137 ATAAAGTGTAAAGCCCTGGGCTGCTAATGAGTGAGCTAACTCACTTAATTTGCGTTGCGC 196
Db 6154 ATAAAGTGTAAAGCCCTGGGCTGCTAATGAGTGAGCTAACTCACTTAATTTGCGTTGCGC 6095
QY 197 TCACCTGCGCGCTTTCAGTCTGGGAAACCTCTGTCGCCAGCTGCATTAATGAATCGGCAA 256
Db 6094 TCACCTGCGCGCTTTCAGTCTGGGAAACCTCTGTCGCCAGCTGCATTAATGAATCGGCAA 6035
QY 257 CGCGCGGGAGAGCGGCTTTCGCTATTTGGCGCCAGGCTGTTTCTTTTCCACAGTGA 316
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QY 377 CAGCGTGGTTTGGCCAGCAGCGGAAATCCTGTTTGTATGTTGCTTCCGAAATCGGAAA 436
Db 5914 CAGCGTGGTTTGGCCAGCAGCGGAAATCCTGTTTGTATGTTGCTTCCGAAATCGGAAA 5855
QY 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGTTTGGAAAC 496
Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGTTTGGAAAC 5795
QY 497 AAGAGTCCACTATTAAGAAGCTGGAATCCAAAGGCGGAAACCGTCTATCAG 556
Db 5794 AAGAGTCCACTATTAAGAAGCTGGAATCCAAAGGCGGAAACCGTCTATCAG 5735
QY 557 GCGGATGGCCACTACGTGAACCATCACCAATCAAGTTTGGGTCGAGGTGCGGT 616
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QY 617 AAAGCACTAAATCGGAACCTTAAGGAGGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 676
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QY 917 TTGAGAAGTGTGTTTATATACAGTGAGCGCACCGAGTAAAGAGTCTGCTCATCAGCAA 976
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QY 1037 ACTCAAACTATCGCCTTGTGTTGATTAATCCAGAACATATACCGCAGCATTGCAAC 1096
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Db 5194 AGGAAAACGCTCATGGAATACCTACATTTTGAGCTCAATCGTCAATGGAATGATTAT 5135
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QY 1157 TACATTGGCAGATTCACAGTCACAGCACAGTAAATAAAGGAGCATCTGCGCCAAACAGA 1216
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Db 5134 TACATTGGCAGATTCACAGTCACAGCACAGTAAATAAAGGAGCATCTGCGCCAAACAGA 5075
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QY 1217 G 1217
Db 5074 G 5074

RESULT 15

US-08-470-297A-2/G
; Sequence 2, Application US/08470297A
; Patent No. 6027933
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,297A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001

; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-470-297A-2

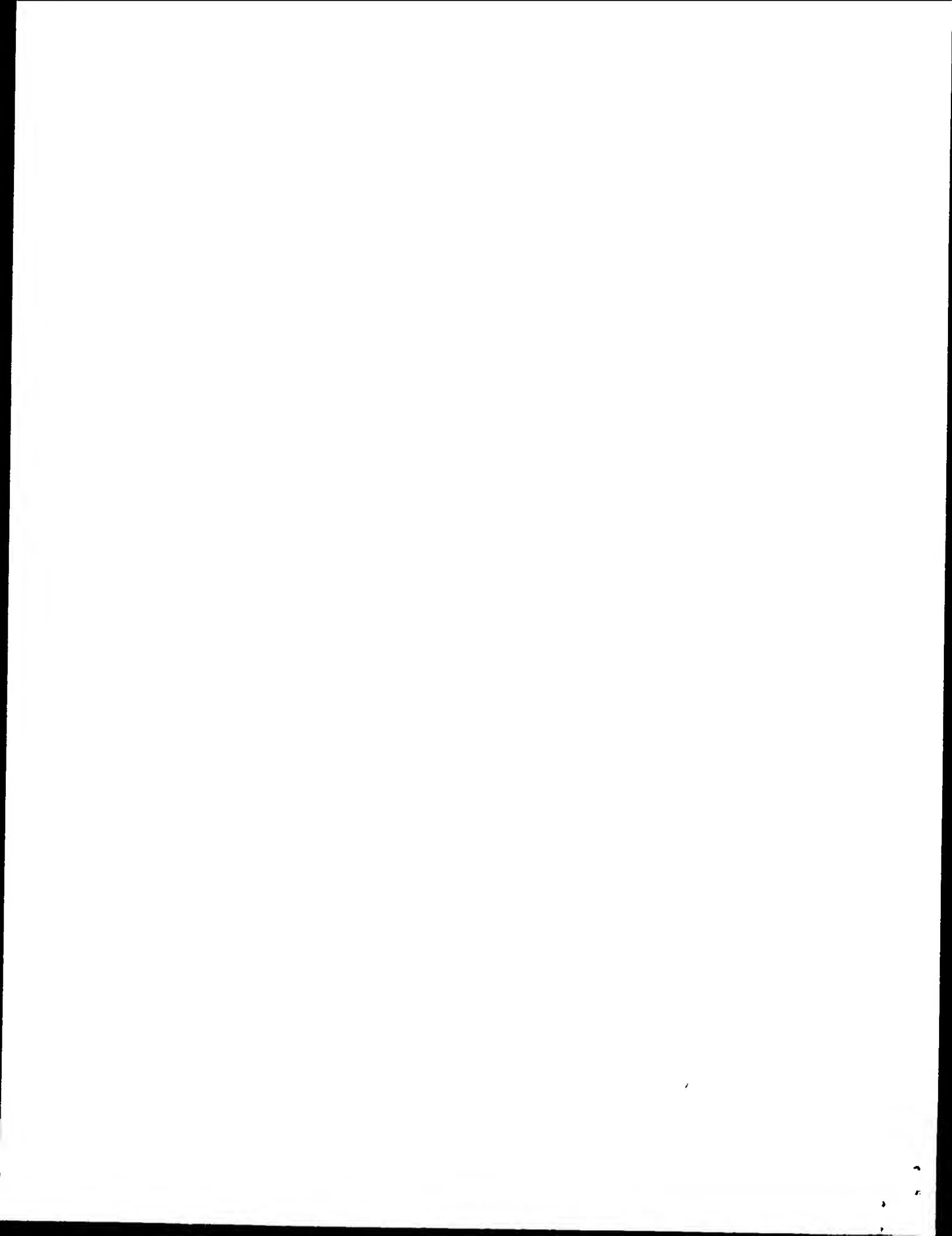
Query Match 93.0%; Score 1131.4; DB 3; Length 7317;
Best Local Similarity 99.5%; Pred. No. 28-242;
Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 77 CTGTTTCTGCTGTGAAATTTATCCGCTCACAATTCACACAACTACGAGCGGGAAGC 136
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Db 6214 CTCCTTGGCGTGTGAATTTGTTATCCGCTCACAATTTCCACACAACTACGAGCGGGAAGC 6155
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QY 137 ATAAAGTGAAGCGCTGGGTGCTTAATGAGTGAGTAACTCACTTAATTTGCTTTCGCG 196
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Db 6154 ATAAAGTGAAGCGCTGGGTGCTTAATGAGTGAGTAACTCACTTAATTTGCTTTCGCG 6095
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QY 197 TCACCTGCGCGCTTTCCAGTCGCGGAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAA 256
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Db 6094 TCACCTGCGCGCTTTCCAGTCGCGGAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAA 6035
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QY 257 CGCGCGGGAGAGCGGCTTTGCGTATTTGGCGCGCAGGGTGGTTTCTTTTACCAGTGA 316
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Db 6034 CGCGCGGGAGAGCGGCTTTGCGTATTTGGCGCGCAGGGTGGTTTCTTTTACCAGCGGA 5975
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QY 317 GACGGGCAACAGCTGATTCGCTTTCACCGCTTGGCCCTGAGAGAGTTGACGAAAGCGGTC 376
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Db 5974 GACGGGCAACAGCTGATTCGCTTTCACCGCTTGGCCCTGAGAGAGTTGACGAAAGCGGTC 5915
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QY 377 CACGCTGTTTGGCCCGCAGCGCAATCTGTTTGTGTTGGTTCGGAATTCGGCAAA 436
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Db 5914 CACGCTGTTTGGCCCGCAGCGCAATCTGTTTGTGTTGGTTCGGAATTCGGCAAA 5855
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QY 437 ATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGTTTCCAGTTTGAAC 496
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Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGTTTCCAGTTTGAAC 5795
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QY 497 AAGAGTCCACTATTAAAGAACGTGACCTCAACGTCACAAAGGCGGAAAAACCGCTATCAG 556
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Db 5794 AAGAGTCCACTATTAAAGAACGTGACCTCAACGTCACAAAGGCGGAAAAACCGCTATCAG 5735
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QY 557 GCGGATGCGCCACACGTAACCATCACCCCAATCAAGTTTGGGGTTCGAGTGGCGCT 616
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QY 617 AAAGCAGTAAATCGGAACCCCTAAAGGGAGCCCGGATTTAGAGCTTTGACGGGAAAGCCG 676
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Db 5674 AAAGCAGTAAATCGGAACCCCTAAAGGGAGCCCGGATTTAGAGCTTTGACGGGAAAGCCG 5615
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QY 677 GCGAACGTGGCGGAGAAAGGAGGAGAAAGGAGGAGGCGGCTAGGGCGCTGGCA 736
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QY 737 AGTGAGCTGCTGCGCTGCGGCTAACACACACCGCGCTTAATCGCGCTACAG 796
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Db 5494 GCGCGCTACTATGTTGCTTTGACGAGCAGCTATAACGCTGCTTCTCTGTTGGAATCAGA 5435
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QY 857 GCGGAGCTAAACAGGAGCGGATTAAGGGATTTTAGACAGAACGGTACGCCAGAATC 916
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Db 5434 GCGGAGCTAAACAGGAGCGGATTAAGGGATTTTAGACAGAACGGTACGCCAGAATC 5375
|||||
QY 917 TTGAGAAGTGTGTTTATATAATCAGTGAGCGCACCGAGTAAAGAGTCTGCTCATCAGCAA 976
|||||
Db 5374 TTGAGAAGTGTGTTTATATAATCAGTGAGCGCACCGAGTAAAGAGTCTGCTCATCAGCAA 5315
|||||

us-10-014-743-1.rni

Thu Aug 1 12:08:39 2002

QY 977 ATTAACCGTTGTAGCAATACTTCTTTGATTAGTAATAACATCACTTGCTGAGTAGAGA 1036
 Db 5314 ATTAACCGTTGTAGCAATACTTCTTTGATTAGTAATAACATCACTTGCTGAGTAGAGA 5255
 QY 1037 ACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACAAATATTACCGCCAGCCATTGCAAC 1096
 Db 5254 ACTCAAACTATCGGCTTGTGCTGTAATATCCAGAACAAATATTACCGCCAGCCATTGCAAC 5195
 QY 1097 AGCAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAAATGGATTATT 1156
 Db 5194 AGCAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAAATGGATTATT 5135
 QY 1157 TACATTGGCAGATTCACCGATCAGACGAGTAAATAAGGGACATTCTGGCCCAACAGA 1216
 Db 5134 TACATTGGCAGATTCACCGATCAGACGAGTAAATAAGGGACATTCTGGCCCAACAGA 5075
 QY 1217 G 1217
 Db 5074 G 5074

Search completed: August 1, 2002, 09:30:47
 Job time: 6608 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 06:51:49 ; Search time 2971.21 Seconds
(without alignments)
5528.318 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAGCTTGCATGCTGCA.....GGACATTCGTGGCAACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthma.*
3: em_estin.*
4: em_estma.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555.4	45.6	687	12	AQ937512 NB6-1069C
2	497.4	40.9	632	10	BI795424 H021C07 E
3	452.4	37.2	478	9	AU014102 AU014102
4	450.2	37.0	571	12	AL002077 F.rubripe
5	433.6	35.6	564	12	AL002058 F.rubripe
6	394.6	32.4	770	12	AQ991774 RfC02039F
7	387.2	31.8	588	12	AL002056 F.rubripe
8	383.4	31.5	677	12	AL441673 T. brucei
9	379.6	31.2	611	9	AJ273684 AJ273684
10	379	31.1	554	12	BH216739 1006046A1
11	379	31.1	556	12	BH231528 1006162F0
12	379	31.1	581	9	AV403804 AV403804
13	379	31.1	584	9	AV404063 AV404063
14	379	31.1	627	9	AV403998 AV403998
15	379	31.1	627	9	AV404060 AV404060
16	379	31.1	627	9	AV404091 AV404091
17	379	31.1	627	9	AV404095 AV404095

18	379	31.1	628	9	AV403779
19	379	31.1	628	9	AV403828
20	379	31.1	628	9	AV403918
21	379	31.1	628	9	AV403919
22	379	31.1	628	9	AV403945
23	379	31.1	628	9	AV403970
24	379	31.1	628	9	AV403997
25	379	31.1	628	9	AV404068
26	379	31.1	629	9	AV404061
27	379	31.1	681	9	AV403811
28	379	31.1	681	9	AV403921
29	379	31.1	684	9	AV404405
30	379	31.1	690	9	AV405131
31	379	31.1	713	9	AV403818
32	379	31.1	724	9	AV404381
33	379	31.1	748	10	BG671706 DRNBG07
34	379	31.1	756	9	AV404290
35	379	31.1	783	9	AV402901
36	379	31.1	786	9	AV404165
37	379	31.1	799	9	AV405326
38	379	31.1	837	9	AV405305
39	378.4	31.1	644	12	AQ115013 CIT-HSP-2
40	378.4	31.1	654	12	B78704 CIT979SK-A-
41	378.4	31.1	659	12	BH244704 ATZEB93TR
42	378.4	31.1	826	12	A2679318 ENTIG84TR
43	378.4	31.1	838	12	A2687181 ENTMP05TR
44	378.4	31.1	841	12	A2541344 ENTFA04TR
45	378.4	31.1	865	12	A2670321 ENTLR28TR

ALIGNMENTS

RESULT 1
AQ937512 AQ937512 687 bp DNA linear GSS 23-AUG-2000
LOCUS NB6-1069C Human NotI clones Homo sapiens genomic, DNA sequence.
DEFINITION AQ937512
ACCESSION AQ937512
VERSION AQ937512.1 GI:7213890
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie,L., Muravenko,O.V., Kozirev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
MEDLINE 20175728
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.
Location/Qualifiers
source
1. .687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
BASE COUNT 168 a 170 c 187 g 162 t
ORIGIN

Query Match 45.6%; Score 555.4; DB 12; Length 687;
Best Local Similarity 99.1%; Pred. No. 2.2e-148;
Matches 570; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
QY 33 AGGATCCCCGGGTACCGAGCTCG----AATTCCTAATCATGGTCATAGCTGTTTCTCTG 88

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Db 113 ATGATCCCGGATACCGAGCTCGAATTAATGTAATCAATGTCATAGCTGTTCTCGTG 172
QY 89 TGAATTTGTTATCGCTCACAAATTCACACACATACAGCGCGGAAGCATAAAGTGTAA 148
Db 173 TGAATTTGTTATCGCTCACAAATTCACACACATACAGCGCGGAAGCATAAAGTGTAA 232
QY 149 GCCTGGGGTGCTTAATGAGTGAGCTCAATTAATGCGTTCCTGCTCACTGCCGCT 208
Db 233 GCCTGGGGTGCTTAATGAGTGAGCTCAATTAATGCGTTCCTGCTCACTGCCGCT 292
QY 209 TTCAGTCGGGAACCTGCTGCTCCAGCTGCAATTAATGAAATCGGCCAAGCGCGGGGAGA 268
Db 293 TTCAGTCGGGAACCTGCTGCTCCAGCTGCAATTAATGAAATCGGCCAAGCGCGGGGAGA 352
QY 269 GGGGTTTGCTATTTGGCGCGCAGGCTGTTTCTTTTCCACAGTGAGCGGGCAACAG 328
Db 353 GGGGTTTGCTATTTGGCGCGCAGGCTGTTTCTTTTCCACAGTGAGCGGGCAACAG 412
QY 329 CTGATTCCTTCCACCGCTGGCCCTGAGAGAGTTGCGAGAGCGGTCCACGCTGGTTTG 388
Db 413 CTGATTCCTTCCACCGCTGGCCCTGAGAGAGTTGCGAGAGCGGTCCACGCTGGTTTG 472
QY 389 CCCAGCAGCGGAAATCCTGTTGATGCTGTTCCGAAATCGGCAAAATCCTTTATAA 448
Db 473 CCCAGCAGCGGAAATCCTGTTGATGCTGTTCCGAAATCGGCAAAATCCTTTATAA 532
QY 449 TCAAAAGATAGCCCGAGATAGGCTGTTGATGCTGTTCCAGTTTGAACAAAGAGTCCACTA 508
Db 533 TCAAAAGATAGCCCGAGATAGGCTGTTGATGCTGTTCCAGTTTGAACAAAGAGTCCACTA 592
QY 509 TTAAGAACGTGGACTCAAGCTCAAGGGCGAAGAACCGTCTATCAGGGCGATGCCCA 568
Db 593 TTAAGAACGTGGACTCAAGCTCAAGGGCGAAGAACCGTCTATCAGGGCGATGCCCA 652
QY 569 CTAGTGAACCATCACCAATCAAGTTTGTGG 603
Db 653 CTAGTGAACCATCACCAATCAAGTTTGTGG 687

RESULT 2
BI795424/c
LOCUS
DEFINITION
H021C07 Endosperm library from Oryza sativa (10 days after anthesis
) Oryza sativa cDNA clone H021C07, mRNA sequence.
ACCESSION
BI795424
VERSION
EST.
KEYWORDS
SOURCE
Oryza sativa.
ORGANISM
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 632)
AUTHORS
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu
H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
TITLE
A Gene Expression Screen in Oryza sativa
JOURNAL
Unpublished (2001)
COMMENT
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268# Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86852051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
FEATURES
Location/Qualifiers
1..632
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="H021C07"
/gene="H021C07"
/gene_lib="Endosperm library from Oryza sativa (10 days
after anthesis)"
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/tissue_type="Endosperm"
/dev_stage="10 days after anthesis"
/note="Vector: pSport2"
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Best Local Similarity 93.7%; Pred. No. 9.9e-132;
Matches 595; Conservative 0; Mismatches 31; Indels 9; Gaps 7;
QY 16 CTGAGGTGCGACTCTAGAGGATCCCGGGTACGAGCTCGAATTCGTAATCATGGTCATA 75
Db 630 CTGAGGTGCGACTCTAGAGGATCCCGGGTACGAGCTCGAATTCGTAATCATGGTCATA 572
QY 76 GCTGTTTCTGTCGCAAAATGTTATCCGCTGCAAAATTCACACACATACGAGCGGGAAG 135
Db 571 GCTGTTTCTGTCGCAAAATGTTATCCGCTGCAAAATTCACACACATACGAGCGGGAAG 512
QY 136 CATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGTTGCG 195
Db 511 CATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGTTGCG 452
QY 196 CTCAGTCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAATTAATGAATTCGCCA 255
Db 451 CTCAGTCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAATTAATGAATTCGCCA 392
QY 256 ACGCGGGGAGAGCGGCTTTGCGTATTCGGCGCCAGGCTGTTTCTTTTCCACCAAGTG 315
Db 391 ACGCGGGGAGAGCGGCTTTGCGTATTCGGCGCCAGGCTGTTTCTTTTCCACCAAGTG 332
QY 316 AGACGGGCAACAGCTGATTGCTTCCAGCTGGCCCTGAGAGAGTTGCGAGCAAGCGGT 375
Db 333 AGACGGGCAACAGCTGATTGCTTCCAGCTGGCCCTGAGAGAGTTGCGAGCAAGCGGT 275
QY 376 CCAGCTGCTTTGCCCGAGCAGCGGCAAAATCTCTGTTGATGTTGTTCCGAAATTCGCCAA 435
Db 274 CCAGCTGCTTTGCCCGAGCAGCGGCAAAATCTCTGTTGATGTTGTTCCGAAATTCGCCAA 216
QY 436 AATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTTGTTCCAGTTTGGAA 495
Db 215 AATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTTGTTCCAGTTTGGAA 156
QY 496 CAAGAGTCCACTATTAAGAGAGCTGGACTCCAAAGTCAAGGGCGGAAACCTCTATCA 555
Db 155 CAAGAGTCCACTATTAAGAGAGCTGGACTCCAAAGTCAAGGGCGGAAACCTCTATCA 98
QY 556 GGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTCGGGGTTCGAGGTGCCG 615
Db 97 GG--CGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTCGGGGTTCGAGGTGCCG 40
QY 616 TAAAGCACTAAATCGGAACCCCTAAAGGGAGGAGCCCC 650
Db 39 GTAAGCACTAAATCGGAACCCCTAAAGGGAGGAGCCCC 5
RESULT 3
AU014102
LOCUS
DEFINITION
AU014102 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc09168, mRNA sequence.
ACCESSION
AU014102
VERSION
AU014102.1 GI:3368893
KEYWORDS
SOURCE
fission yeast.
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE
1 (bases 1 to 478)
AUTHORS
Morimoto, M. and Mita, K.
TITLE
Identification of expressed sequence tags of Schizosaccharomyces
pombe
```

Unpublished (1998)
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp
Location/Qualifiers
1. 478
/organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone_lib="spc09168"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

BASE COUNT 143 a 108 c 138 g 86 t 3 others
ORIGIN

Query Match 37.2%; Score 452.4; DB 9; Length 478;
Best Local Similarity 97.0%; Pred. No. 7.4e-119;
Matches 459; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 450 CAAAGAATAGCCGAGATAGGTTGAGTGTGTTCCAGTTTGGACACAGAGTCCACTAT 509
Db 6 CGAATAAATAAATAATAGGTTGAGTGTGTTCCAGTTTGGACACAGAGTCCACTAT 65
QY 510 TAAAGAACGTGGACTCAACGTCAGAGGGGCAAAACCCGTCATCAGGGCGATGGCCAC 569
Db 66 TAAAGAACGTGGACTCAACGTCAGAGGGGCAAAACCCGTCATCAGGGCGATGGCCAC 125
QY 570 TAGCTGAACCATCACCAATCAAGTTTGTGGGCTCGAGTGCCTGTAAGACACTAAATC 629
Db 126 TAGCTGAACCATCACCAATCAAGTTTGTGGGCTCGAGTGCCTGTAAGACACTAAATC 185
QY 630 GGAACCCCTAAAGGAGCCCGCATTTAGAGCTTGACGGGGAAGCCGCGAAGCTGGGA 689
Db 186 GGAACCCCTAAAGGAGCCCGCATTTAGAGCTTGACGGGGAAGCCGCGAAGCTGGGA 245
QY 690 GAAAGGAAGGAAGAAAGAGGCGGCTAGGCGCTGCAAGTGTAGCGGTCA 749
Db 246 GAAAGGAAGGAAGAAAGAGGCGGCTAGGCGCTGCAAGTGTAGCGGTCA 305
QY 750 CGCTGCGGCTAACCCACACACCCCGCGCTTAATGCGCGCTACAGGCGCGTACTATG 809
Db 306 CGCTGCGGCTAACCCACACACCCCGCGCTTAATGCGCGCTACAGGCGCGTACTATG 365
QY 810 GTTGTCTTACGAGCAGTATTAAGCTGTTTCCCTGTTGGAATCAGAGCGGAGCTAAAC 869
Db 366 GTTGTCTTACGAGCAGTATTAAGCTGTTTCCCTGTTGGAATCAGAGCGGAGCTAAAC 425
QY 870 AGGAGGCGGATTAAGGATTTTACAGAGGAACGGTACGCCAGATCTTGAGA 922
Db 426 AGGAGGCGGATTAAGGATTTTACAGAGGAACGGTACGCCAGATCTTGAGA 478

RESULT 4
FR0010806 571 bp DNA linear GSS 18-SEP-1997
LOCUS F.rubripes GSS sequence, clone 045G19ah11, genomic survey sequence.
DEFINITION AL002077
ACCESSION AL002077.1 GI:2447647
VERSION GSS; genome survey sequence.
KEYWORDS Takifugu rubripes.
SOURCE Takifugu rubripes.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.
1 (bases 1 to 571)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umraniya, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
Vector: m13mp18
V.type: phage
PRIMER: M13
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic sequence.
Location/Qualifiers
1. 571
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid_045G19"
/clone="045G19ah11"

BASE COUNT 161 a 130 c 159 g 109 t 12 others
ORIGIN

Query Match 37.0%; Score 450.2; DB 12; Length 571;
Best Local Similarity 90.7%; Pred. No. 3.4e-118;
Matches 517; Conservative 0; Mismatches 49; Indels 4; Gaps 4;

QY 333 TTGCCCTTCACCGCTGCGCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGTTGTCGCC 392
Db 1 TTGCCCTTCACCGCTGCGCTGAGAGAGTTGCAGCAAGCGGTCCAC -CTGCTTGC 58
QY 393 AGCAGGCGAAATTCCTGTTGATGTTGTCGAAATCGGCAAAATCCCTTATAATCAA 452
Db 59 AGCAGGCGAAATTCCTGTTGATGTTGTCGAAATCGGCAAAATCCCTTATAATCAA 118
QY 453 AAGATACCCCGAGATAGGTTGAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATAA 512
Db 119 AAGATACCCCGAGATAGGTTGAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATAA 178
QY 513 AGAAGCTGGACTCCCAAGCTCAAGGGCGAAACCCGCTTATCAGGCGGATGGCCACTAC 572
Db 179 AGAAGCTGGACTCCCAAGCTCAAGGGCGAAACCCGCTTATCAGGCGGATGGCCACTAC 238
QY 573 GTGAACCATCACCAATCAAGTTTTCGGGTCGAGGTGCGCTTAAGCACTAAATCGGA 632
Db 239 GTGAACCATCACCAATCAAGTTTTCGGGTCGAGGTGCGCTTAAGCACTAAATCGGA 298
QY 633 ACCCTAAAGGGAGCGCCCGATTTAGAGCTTGACGGGGAAGCCGCGAAGCTGGCGAGAA 692
Db 299 ACCCTAAAGGGAGCGCCCGATTTAGAGCTTGACGGGGAAGCCGCGAAGCTGGCGAGAA 358
QY 693 AGGAAGGGAAGAAAGCGAGCGGCTAGGCGGCTAGGCGGCTAGGCGGCTAGGCGGCTACGC 752
Db 359 AGGAAGGGAAGAAAGCGAGCGGCTAGGCGGCTAGGCGGCTAGGCGGCTAGGCGGCTACGC 417
QY 753 TCGCGGTACCCACACACCGCGCTTAATCGCGCTACAGGGCGGCTACTATGCTT 812
Db 418 TCGCGGTACCCACACACCGCGCTTAATCGCGCTACAGGGCGGCTACTATGCTT 477
QY 813 GCTTTCAGGACGACGTATAACGTCCTTCTCTGTTTGAATCAGAGCGGGAGCTAAACAGG 872
Db 478 GCTTTCAGGACGACGTATAACGTCCTTCTCTGTTTGAATCAGAGCGGGAGCTAAACAGG 537
QY 873 AG-GCCGATTAAGGATTTTACAGAGGAA 901
Db 538 AGNGCCGATTAAGGATTTTANACAGNGA 567

RESULT 5
FR0010787 564 bp DNA linear GSS 18-SEP-1997
LOCUS F.rubripes GSS sequence, clone 045G19ac4, genomic survey sequence.
DEFINITION AL002058
ACCESSION AL002058

VERSION AL002058.1 GI:2447628
 KEYWORDS GSS, genome survey sequence.
 SOURCE Takifugu rubripes.
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Takifugu.

REFERENCE 1 (bases 1 to 564)
 AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y.,
 Williams, G. and Brenner, S.
 TITLE Direct Submission
 JOURNAL Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
 COMMENT Vector: m13mp18
 V-type: phage
 PRIMER: M13

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
 sequence.

FEATURES Location/Qualifiers
 source 1..564
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 /db_xref="taxon:31033"
 /clone_lib="cosmid 045G19"
 /clone="045G19aC4"
 BASE COUNT 159 a 129 c 159 g 112 t 5 others
 ORIGIN

Query Match 35.6%; Score 433.6; DB 12; Length 564;
 Best Local Similarity 94.0%; Pred. No. 2e-113;
 Matches 535; Conservative 0; Mismatches 24; Indels 10; Gaps 8;

QY 338 CTTACCCGCTGGCCCTGAGAGAGTTGCAGCAGCGGTCCAGCGTGTGTCGCCAGCAG 397
 Db 1 CTTACCCGCTGGCCCTGAGAGAGTTGCAGCAGCGGTCCAC-NTGGTTGGCCCGCAGCAG 59

QY 398 GCGAAATCCCTGTTGATGTTGTTCCGAATCGCAAAATCCCTTATAATCAAAAGAA 457
 Db 60 GCGAAATCCCTGTTGATGTTGTTCCGAATCGCAAAATCCCTTATAATCAAAAGAA 119

QY 458 TAGCCCGAGATAGGTTGATGTTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAAC 517
 Db 120 TAGCCCGAGATAGGTTGATGTTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAAC 179

QY 518 GTGACTCCAACTCAAGGCGCAAAACCGTCTATCAGGCGGATGGCCCACTACGTGAA 577
 Db 180 GTGACTCCAACTCAAGGCGCAAAACCGTCTATCAGGCGGATGG-CCACTACGTGAA 238

QY 578 CCATCACCCAAATCAAGTTTGGGTGCGAGGTGCGGTAAAGCAGTAAATCGGAACCT 637
 Db 239 CCATCACCCAAATCAAGTTTGGGTGCGAGGTGCGGTAAAGCAGTAAATCGGAACCT 298

QY 638 AAAGGGAGCCCGATTTAGAGCTTACGCGGAAAGCGGCGGAAAGCGGCGGAGAAAGAA 697
 Db 299 AAAGGGAGCCCGATTTAGAGCTTACGCGGAAAGCGGCGGCGGAGAAAGCGGCGGAGAAAGAA 358

QY 698 GGAAGAAAGCGAAAGGAGCGGCGCTAGGCGCTGCGCAAGTGTAGCGGTACCGCTGCGC 757
 Db 359 GGAAGAAAGCGAAAGGAGCGGCGCTAGGCGCTGCGCAAGTGTAGCGGTACCGCTGCGC 416

QY 758 GTAACCAACACCCCGCGCTTAATGCGCGCTACAGGCGCGGTACTATGTTGC-TT 816
 Db 417 TAAACCAACACCCCGCGCTTAATGCGCGCTACAGGCGCGGTACTATGTTGC-TT 475

QY 817 TGACGAGCAGTATAAGCTGCTTCTCGTTGGAAT--CAGACGGGAGTAACAGGAG 874
 Db 476 TGACGAGCAGTATAAGCTTCTCGTTGGAAT--CAGACGGGAGTAACAGGAG 448

QY 875 G--CCGATTAAAGGGATTTAGACAGGAA 901
 Db 536 GGCCCGATTAAAGGGATTTAGACAGGAA 564

RESULT 6

AQ991774
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

TITLE

JOURNAL
 MEDLINE
 COMMENT

AQ991774 770 bp DNA linear GSS 14-AUG-2000
 Rf02039F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02039F, DNA sequence.
 AQ991774
 AQ991774.1 GI:9650368
 GSS.
 Photorhabdus luminescens.
 Photorhabdus luminescens.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Photorhabdus.
 1 (bases 1 to 770)
 fFrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14; potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk

This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see fFrench-Constant et al.
 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES Location/Qualifiers
 1..770
 /organism="Photorhabdus luminescens"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02039F"
 /clone_lib="Photorhabdus luminescens strain W14 M13
 library"
 /dev_stage="primary phase variant"
 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janus."

BASE COUNT 238 a 166 c 178 g 165 t 23 others
 ORIGIN

Query Match 32.4%; Score 394.6; DB 12; Length 770;
 Best Local Similarity 84.9%; Pred. No. 3.6e-102;
 Matches 478; Conservative 0; Mismatches 74; Indels 11; Gaps 4;

QY 368 CAAGCGTCCAGCGTGTGTCGCCAGCAGCGGAAATCCTGTTGATCGTGTTCGAA 427
 Db 209 CAAGCGTCCAGCGTGTGTCGCCAGCAGCGGAAATCCTGTTGATCGTGTTCGAA 268

QY 428 ATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTTGTTCCA 487
 Db 269 ATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTTGTTCCA 328

QY 488 GTTTGGACAAAGTCCACTATTAAAGAACGTGGACTCCAAGTCAAGGGCGGAAACCC 547
 Db 329 GTTTGGACAAAGTCCACTATTAAAGAACGTGGACTCCAAGTCAAGGGCGGAAACCC 388

QY 548 GTCTATCAGGGCGATGGCCCACTACCTCAACCATCACCAATCAAGTTTGGGGTCC 607
 Db 389 GTCTATCAGGGCGATGGCCCACTACCTCAACCATCACCAATCAAGTTTGGGGTCC 448

QY 608 AGGTGCGTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGCCGATTAGAGCTTGACGG 667
 Db 449 AGGNGCGTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGCCGATTAGAGCTTGACGG 508

and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 163 a 123 c 146 g 122 t
ORIGIN

Query Match 31.1%; Score 379; DB 12; Length 554;
Best Local Similarity 97.5%; Pred. No. 9.6e-98;
Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
|||||
Db 75 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 134
|||||

Qy 483 TTCAGTTTGGCAACAGATCCATATTAAGACGTGGACTCCACGTCACAAAGGCGGAA 542
|||||
Db 135 TTCAGTTTGGCAACAGATCCATATTAAGACGTGGACTCCACGTCACAAAGGCGGAA 194
|||||

Qy 543 AAACCGTCTATCAGGGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGG 602
|||||
Db 195 AAACCGTCTATCAGGGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGG 254
|||||

Qy 603 GGTGAGGTGCGGTAAGACACTAAATCGGAACCCCTAAAGGAGGCGCCCGATTAGAGCTT 662
|||||
Db 255 GGTGAGGTGCGGTAAGACACTAAATCGGAACCCCTAAAGGAGGCGCCCGATTAGAGCTT 314
|||||

Qy 663 GACGGGAAAGCCCGGACGTGGCGAGAGAGGAGGAAAGCGAAAGGAGGCGGCG 722
|||||
Db 315 GACGGGAAAGCCCGGACGTGGCGAGAGAGGAGGAAAGCGAAAGGAGGCGGCG 374
|||||

Qy 723 CTAGGGCGCTGCGAAGTGTACGCTGCGGCTAACACACACACCGCGCGCTTA 782
|||||
Db 375 CTAGGGCGCTGCGAAGTGTACGCTGCGGCTAACACACACACCGCGCGCTTA 434
|||||

Qy 783 ATGCGCGCTACAGGGCGGCTACTATGTTGCTTT 817
|||||
Db 435 ATGCGCGCTACAGGGCGGCTACTATGTTGCTTT 469
|||||

RESULT 11
BH231528
LOCUS 1006162F02.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
DEFINITION
ACCSSION
BH231528
VERSION
BH231528.1 GI:16835766
KEYWORDS
GSS.
SOURCE
ORGANISM
Zea mays.
Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon (Unpublished (2001))
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1006162 row: 19
Class: transposon-tagged.
Location/Qualifiers
1..556
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AV403804
AV403804 Bombyx mori pheromone gland Shuko x Ryuhaku newly-closed adult Bombyx mori cDNA clone pg--0075 T3, mRNA sequence.
AV403804
AV403804.1 GI:6907892
EST.
KEYWORDS
SOURCE
ORGANISM
Bombyx mori
domestic silkworm.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 581)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences

RESULT 12
AV403804
LOCUS
DEFINITION
ACCSSION
AV403804
VERSION
AV403804.1 GI:6907892
KEYWORDS
SOURCE
ORGANISM
Bombyx mori
domestic silkworm.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 581)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences

/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 160 a 121 c 145 g 128 t 2 others
ORIGIN

Query Match 31.1%; Score 379; DB 12; Length 556;
Best Local Similarity 97.5%; Pred. No. 9.6e-98;
Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
|||||
Db 96 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 155
|||||

Qy 483 TTCCAGTTTGGCAACAGATGCCACTATTAAAGAACGTGGACTCCACGTCACAAAGGCGGAA 542
|||||
Db 156 TTCCAGTTTGGCAACAGATGCCACTATTAAAGAACGTGGACTCCACGTCACAAAGGCGGAA 215
|||||

Qy 543 AAACCGTCTATCAGGGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGG 602
|||||
Db 216 AAACCGTCTATCAGGGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGG 275
|||||

Qy 603 GGTGAGGTGCGGTAAGACACTAAATCGGAACCCCTAAAGGAGGCGGCGCTTTAGAGCTT 662
|||||
Db 276 GGTGAGGTGCGGTAAGACACTAAATCGGAACCCCTAAAGGAGGCGGCGCTTTAGAGCTT 335
|||||

Qy 663 GACGGGAAAGCCCGGACGTGGCGAGAGGAGGAAAGCGAAAGGAGGCGGCG 722
|||||
Db 336 GACGGGAAAGCCCGGACGTGGCGAGAGGAGGAAAGCGAAAGGAGGCGGCG 395
|||||

Qy 723 CTAGGGCGCTGCGAAGTGTACGCTGCGGCTAACACACACACCGCGCGCTTA 782
|||||
Db 396 CTAGGGCGCTGCGAAGTGTACGCTGCGGCTAACACACACACCGCGCGCTTA 455
|||||

Qy 783 ATGCGCGCTACAGGGCGGCTACTATGTTGCTTT 817
|||||
Db 456 ATGCGCGCTACAGGGCGGCTACTATGTTGCTTT 490
|||||

RESULT 12
AV403804
LOCUS
DEFINITION
ACCSSION
AV403804
VERSION
AV403804.1 GI:6907892
KEYWORDS
SOURCE
ORGANISM
Bombyx mori
domestic silkworm.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 581)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences

Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
 Email: knita@nirs.go.jp
 Method: uni-directional, sequence direction: sequenced from T3 primer
 (5' -> 3')
 Project: 'Silkworm Genome Program in MAFF, and Research for the
 Future Program in JSPS'. see 'SilkBase',
 <http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

Location/Qualifiers
 1. 581
 /organism="Bombyx mori"
 /strain="Shuko x Ryuhaku"
 /db_xref="taxon:7091"
 /clone="pg--0075"
 /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
 newly-enclosed adult"
 /sex="female"
 /tissue_type="pheromone gland"
 /dev_stage="newly-enclosed adult"
 166 a 131 c 151 g 133 t

BASE COUNT
 ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 581;
 Best Local Similarity 97.5%; Pred. No. 9.8e-98;
 Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGTG 482
 DB 116 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGTG 175
 QY 483 TTCACGTTTGGACAAAGTCCACTATTAAGAAGCTGGACTCCAACTCAAGGCGGAA 542
 DB 176 TTCACGTTTGGACAAAGTCCACTATTAAGAAGCTGGACTCCAACTCAAGGCGGAA 235
 QY 543 AAACCGTCTATCAGGGGATGGCCACTACCTGAACCATCACCCAAATCAAGTTTTTGG 602
 DB 236 AAACCGTCTATCAGGGGATGGCCACTACCTGAACCATCACCCAAATCAAGTTTTTGG 295
 QY 603 GGTGAGGTGCGTAAAGACCTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGCTT 662
 DB 296 GGTGAGGTGCGTAAAGACCTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGCTT 355
 QY 663 GACGGGAAAGCGGCAAGCTGCGGAGAAAGGAGGAAAGAGCGAAGGAGCGGGCG 722
 DB 356 GACGGGAAAGCGGCAAGCTGCGGAGAAAGGAGGAAAGAGCGAAGGAGCGGGCG 415
 QY 723 CTAGGCGCTGGCAAGGTAGCGGTACGCTGCGGCTAACCCACACCGCGCGCTTA 782
 DB 416 CTAGGCGCTGGCAAGGTAGCGGTACGCTGCGGCTAACCCACACCGCGCGCTTA 475
 QY 783 ATCGCGCGCTACAGGGCGGCTACTATGTTGCTTT 817
 DB 476 ATCGCGCGCTACAGGGCGGCTAGTGGCTTT 510

RESULT 13

AV404063
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Bombyx mori
 domestic silkworm.
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
 1 (bases 1 to 584)
 BOMBYCOIDEA; Bombycidae; Bombyx.
 Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
 Bombyx mori CDNA
 Unpublished (2000)
 Contact: Mita K

Genome Research Group
 National Institute of Radiological Sciences
 Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
 Email: knita@nirs.go.jp
 Method: uni-directional, sequence direction: sequenced from T3 primer
 (5' -> 3')
 Project: 'Silkworm Genome Program in MAFF, and Research for the
 Future Program in JSPS'. see 'SilkBase',
 <http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

Location/Qualifiers
 1. 584
 /organism="Bombyx mori"
 /strain="Shuko x Ryuhaku"
 /db_xref="taxon:7091"
 /clone="pg--0399"
 /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
 newly-enclosed adult"
 /sex="female"
 /tissue_type="pheromone gland"
 /dev_stage="newly-enclosed adult"
 167 a 133 c 151 g 133 t

BASE COUNT
 ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 584;
 Best Local Similarity 97.5%; Pred. No. 9.8e-98;
 Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGTG 482
 DB 117 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGTG 176
 QY 483 TTCACGTTTGGACAAAGTCCACTATTAAGAAGCTGGACTCCAACTCAAGGCGGAA 542
 DB 177 TTCACGTTTGGACAAAGTCCACTATTAAGAAGCTGGACTCCAACTCAAGGCGGAA 236
 QY 543 AAACCGTCTATCAGGGGATGGCCACTACCTGAACCATCACCCAAATCAAGTTTTTGG 602
 DB 237 AAACCGTCTATCAGGGGATGGCCACTACCTGAACCATCACCCAAATCAAGTTTTTGG 296
 QY 603 GGTGAGGTGCGTAAAGACCTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGCTT 662
 DB 297 GGTGAGGTGCGTAAAGACCTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGCTT 356
 QY 663 GACGGGAAAGCGGCAAGCTGCGGAGAAAGGAGGAAAGAGCGAAGGAGCGGGCG 722
 DB 357 GACGGGAAAGCGGCAAGCTGCGGAGAAAGGAGGAAAGAGCGAAGGAGCGGGCG 416
 QY 723 CTAGGCGCTGGCAAGGTAGCGGTACGCTGCGGCTAACCCACACCGCGCGCTTA 782
 DB 417 CTAGGCGCTGGCAAGGTAGCGGTACGCTGCGGCTAACCCACACCGCGCGCTTA 476
 QY 783 ATCGCGCGCTACAGGGCGGCTACTATGTTGCTTT 817
 DB 477 ATCGCGCGCTACAGGGCGGCTAGTGGCTTT 511

RESULT 14

AV403998
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Bombyx mori
 domestic silkworm.
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
 1 (bases 1 to 627)
 BOMBYCOIDEA; Bombycidae; Bombyx.
 Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
 Bombyx mori CDNA

JOURNAL
COMMENT

Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmits@nirs.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3')
Project= 'Silkworm Genome Program in MAFF, and Research for the
Future Program in JSPS', see 'SilkBase',
<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1. 627
/organism="Bombyx mori"
/strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone_pg="pg-0317"
/clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
newly-eclosed adult"
/sex="female"
/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"

BASE COUNT 188 a 137 c 158 g 144 t
ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 627;

Best Local Similarity 97.5%; Pred. No. 1e-97;

Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 482
|||||
Db 116 CCGAAATCGCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 175
QY 483 TTCCAGTTTGGACACAGTCCACTATTAAGAAGCTGGACTCCCAAGCTCAAGGCGCAA 542
Db 176 TTCCAGTTTGGACACAGTCCACTATTAAGAAGCTGGACTCCCAAGCTCAAGGCGCAA 235
QY 543 AAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCAAATCAAGTTTGTG 602
Db 236 AAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCAAATCAAGTTTGTG 295
QY 603 GGTCGAGGTCCGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 662
Db 296 GGTCGAGGTCCGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 355
QY 663 GACGGGAAAGCGCGCGAAGCTGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 356 GACGGGAAAGCGCGCGAAGCTGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 723 CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 782
Db 416 CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 475
QY 783 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 817
Db 476 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 510

RESULT 15

AV404060

LOCUS

AV404060 Bombyx mori pheromone gland Shuko x Ryuhaku mRNA lineair EST 06-FEB-2000
adult Bombyx mori cDNA clone pg-0393 T3, mRNA sequence.

DEFINITION

AV404060

AV404060

VERSION

AV404060.1

KEYWORDS

SOURCE

ORGANISM

Bombyx mori

domestic silkworm.

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia

; Bombycoidea; Bombycidae; Bombyx.

REFERENCE

1 (bases 1 to 627)

AUTHORS
TITLE
JOURNAL
COMMENT

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmits@nirs.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3')
Project= 'Silkworm Genome Program in MAFF, and Research for the
Future Program in JSPS', see 'SilkBase',
<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1. 627
/organism="Bombyx mori"
/strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone_pg="pg-0393"
/clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
newly-eclosed adult"
/sex="female"
/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"

BASE COUNT 188 a 137 c 158 g 144 t
ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 627;

Best Local Similarity 97.5%; Pred. No. 1e-97;

Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 482
Db 116 CCGAAATCGCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 175
QY 483 TTCCAGTTTGGACACAGTCCACTATTAAGAAGCTGGACTCCCAAGCTCAAGGCGCAA 542
Db 176 TTCCAGTTTGGACACAGTCCACTATTAAGAAGCTGGACTCCCAAGCTCAAGGCGCAA 235
QY 543 AAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCAAATCAAGTTTGTG 602
Db 236 AAACCGTCTATCAGGGCGATGGCCACTAGTGAACCATCACCCAAATCAAGTTTGTG 295
QY 603 GGTCGAGGTCCGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 662
Db 296 GGTCGAGGTCCGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 355
QY 663 GACGGGAAAGCGCGCGAAGCTGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 356 GACGGGAAAGCGCGCGAAGCTGCGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 723 CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 782
Db 416 CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 475
QY 783 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 817
Db 476 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 510

Search completed: August 1, 2002, 08:39:40

Job time: 6471 sec

